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Database
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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seq length:
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//SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

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3194
1 MKREYQDAGGSGG
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Arabidopsis thalia	AAG50885	21	541	13.7	439	5
0	AAB28602	21	808	•		4
S	AAB28586	21	809	13.9	443	ω
9	AAB32809	21	113		448	2
Arabidopsis SCAREC.	AAW38181	18	352	•	458	μ
	AAB28603	21	323	•	462.5	0
0	AAB28596	21	352	٠	464	9
	AAG21047	21	593	٠	498	8
Arabidopsis thalia	AAG21048	21	578		498	37
Arabidopsis thalia	AAG21049	21	480	٠	498	8
	AAB28598	21	306	15.8	506	Ğ
Arabidopsis SCLa4.	AAB28570	21	306	٠	507	4
dopsis	AAW38179	18	306	٠	507	ü
SCLm1.	AAB28573	21	313		512	2
Zm-Scl2	AAW38209	18	313	٠	512	<u>=</u>
•	AAB28577	21	313		513	ö
	AAG48516	21	405	٠	523.5	
	AAG29708	21	413		554	8
	AAG29709	21	405		554	27
	AAG29710	21	384	٠	554	86
Arabidopsis thalia	AAW30794	18	259	•	569.5	ŝ
Arabidopsis thalia	AAW30795	18	282	•	589.5	24
'n	AAW81753	19	428	•	599	ະ
	AAB28569	21	653	18.8	600.5	2
opsis SCA	AAW38178	18	653	•	600.5	22
	AAB28595	21	899	•	670	õ
ο.	AAY02544	20	138	•	73	9
	AAW38194	18	262	25.0	97	8
· Arabidopsis SCAREC	AAW38193	18	277	•	812.5	7
oded b	AAY02538	20	256	•	83	9
dopsis SČLa8	AAB28574	21	587	•	LЛ	տ
acid	AAB31884	22	572	49.1	1568	4
d sequen	3188	22	572		1572	$\overline{\omega}$
Arabidopsis SCLa2.	AAB28575	21	531	49.7	1588.5	ฉ

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## ALIGNMENTS

RESULT AAY02540

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AAY02540 standard; Protein; 623

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New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                   WPI; 1999-181040/15.
N-PSDB; AAX36279.
                                                                                                              07-AUG-1998;
                                                                                                                                                WO9909174-A1.
                                                                                                                                                                Triticum aestivum.
                                                                                                                                                                                  paclobutrazol.
                                                          Harberd NP, Peng J, Richards DE;
                                                                             (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                             13-AUG-1997;
                                                                                                                               25-FEB-1999.
                                                                                              97GB-0017192.
                                                                                                              98WO-GB02383
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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;

Protein encoded by wheat Rht clone 5al genomic sequence.

16-JUL-1999 (first entry)

AAY02540;

Score 3194 2683 2189 1612 1612 1594 1594 1590 1590 100.0 84.0 68.5 50.5 50.5 49.9 49.9 49.8 49.8 Match Query Length DВ 20 20 20 22 21 21 21 21 21 ij AAE02560 AAE01892 AAW30792 AAG38575 AAE02545 AAE01907 AAG38577 AAY02540 AAY02541 AAY02539 Protein encoded by Protein encoded by Protein encoded by A. thaliana transc Arabidopsis thalia Description

Result

Pred. No. is the score greater the and is derived be

is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

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AAY02541
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Best Local
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  AAY02541
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                                                                                                                                                                                                                                       GCLTLGWHTRPLIATSAWRLAGP 623
                                                                                                                                        VVACEGAERTERHETLGQWRNRLGNAGFETVHLGSNAYKQASTLLALFAGGDGYKVEEKE
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                                                                    gcltlgwhtrpliatsawrlagp
                                                                                                                                                                                   tfldrfteslhyystmfdsleggssgggpsevssgaaaapaaagtdqvmsevylgrqicn
                                                                                                                                                                                                TFLDRETESLHYYSTMFDSLEGGSSGGGPSEVSSGAAAAPAAAGTDQVMSEVYLGRQICN
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                                                                                                                                                                                                                                                                                                                                                       afadllhahfyescpylkfahftangaileafagcrrvhvvdfgikggmqwpallqalal
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  standard;
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Best Local Similarity
Matches 546; Conserv
                                                                                                                                                                                                                                                                                                                                                                         The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds the major last grow tall. The present sequence is encoded by the major last grow tall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
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                               176
                                                                                                                                                                                                    QKLEQLEMAMGMGGV-GAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPPPL
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   DTQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALARR
                           ppatpaprl-astsstvtsgaaagagyfdlppavdsssstyalkpipspvaaps-adpst 175
                                                                                                     P---PAPQLNASTSSTVT----GSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSA 169
                                                                                                                                             qkleqlemamgmggvggagataddgfvshlatdtvhynpsdlsswvesmlselnappapl
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                                                                                                                                                                                                                                                               84.0%; Score 2683; DB 20;
85.8%; Pred. No. 1.1e-203;
Live 27; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                  clone
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants
                                                                                                                                                                               WPI; 1999-181040/15.
N-PSDB; AAX36278.
                                                                                                                                                                                                                                                                                                                                                                                            Rht gene; homologue; Triticum aestivum; wheat; growth antagonist; gibberellin; dwarf phenotype; gibberellin
                                                                                                                              New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                       Disclosure; Fig 7b; 88pp; English.
                                                                                                                                                                                                                                                               13-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLVAATLADLEPFMLQPEGEEDPNEEPEVIAVNSVFEMHRLLAQPGALEKVLGTVRAVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQVMSEVYLGRQICNVVACEGAERTERHETLGQWRNRLGNAGFETVHLGSNAYKQASTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt glvaatladlepfmlqpeg-ddtddepeviavnsvfelhrllaqpgalekvlgtvravrp}
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                                                                                                                                                                                                                  ΝP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                Peng J,
                                                                                                                                                                                                                                                               97GB-0017192.
                                                                                                                                                                                                                                                                                       98WO-GB02383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 425
                                                                                                                                                                                                                  Richards
                                                                                                                                                                                                                  DE
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                                                                                                                                                                                                                                                                                                                                                                                             inhibition;
biosynthesis;
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RESULT
AAE02560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888888%&
Query Match
Best Local S
Matches 425
                                                                                                                                                                                                                                 transgenic plant; plant yield; growth; germination; photosynthesis; glyvxylate metabolism; respiration; pathogen response; wounding respiration; pigmentation; flowering; senescence; physiological cycle regulation; pigmentation; pigmentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the wheat Rht clone C15-1 cDNA sequence.
                                                                                                                                       Key
Domain
                                                                                                                                                                                                             Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE02560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE02560 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Simhes 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLAGP 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DETDALQQVGWKLAQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGEEDPNEEPEVIAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sleggssgggpsevssgaaaapaaagtdqvmsevylgrqicnvvacegaerterhetlgq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLEGGSSGGGPSEVSSGAAAAPAAAGTDQVMSEVYLGRQICNVVACEGAERTERHETLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt svfemhrllaqpgalekvlgtvravrprivtvveqeanhnsgtfldrfteslhyystmfd}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVFEMHRLLAQPGALEKVLGTVRAVRPRIVTVVEQEANHNSGTFLDRFTESLHXYSTMFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detdalqqvgwklaqfahtirvdfqyrglvaatladlepfmlqpegeedpneepeviavn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.5%; Score 2189; DB 20; ilarity 100.0%; Pred. No. 7.3e-165; Conservative 0; Mismatches 0;
                                                                                                                                                                                                               thaliana
                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor G308 homolog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑA;
                                                                                                                                    Location/Qualifiers 323..339
                                                                                                                "Conserved domain"
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                                                                                                                                                                                                                                                                                                                                                                                                           G307.
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                                                                                                                                                                                                                                                                                   physiology;
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25-MAY-2001

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Best Local Similarity
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17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                            respiration, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, pigmentation, flowering and senescence of plants and for modifying sink-source relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oliseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. The present sequence is a homolog of Arabidopsis thaliana transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the cDNAs and proteins of the invention are useful for modifying the growth and germination rates of plants, photosynthesis, glyoxylate metabolism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang
Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PINE/)
(PILG/)
(ADAM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 115-117; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-335977/35.
N-PSDB; AAD06661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JIAN/)
(HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-2000; 2000WO-US31414.
                                                                                                                                                                                                                                                                                                                                                    Sequence
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   158
                                                                                                115 PLPPAPQLNASTSSTVTGSGGYFDLPPSVD---SSSSIYALRPIPSPAGATAPA-DLSAD 170
                                                                                                                                     61
                                                                                                                                                                                                                    1 MKREYQDAGG----SGGGGGGMCSSEDKMMV--SAAAGEGEEVDELLAALGYKVRASDMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patent relates to polynucleotides encoding 35 plant transcription
                                                                                                                                evalkleqletmm-----snvqedglshlatdtvhynpselyswldnmlseln--pp
                                                                                                                                                    mkrdhhqfqgrlsnhqtssssssiskdkmmmvkkeedgggnmddellavlgykvrssema
snnqnkrlkscsspdsmvtststgtqiggvigttvttttttttaaaestrs--vilvdsq
                                SVRDPKRMRTGGSSTS--SSSSSSSSSLGGGARSSVVEAAPPVAAAANATPALPVVVVDTQ
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                                                                                                                                                                                                                                                                       340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) JIANG C.
) HEARD J.
) PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Heard J,
Samaha R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILGRIM M.
ADAM L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAMAHA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIECHMANN J L.
YU G.
                                                                                                                                                                                                                                                                                                                                                      587 AA;
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2000US-0197899.
2000US-0227439.
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                    50.5%;
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                                                                 -assngldpvlpspeicgfpasdydlkvipgnaiyqfpaidssss
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                                                                                                                                                                                                                                                                   Score 1612; DB 22;
Pred. No. 4.7e-119;
32; Mismatches 149;
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                                                                                                                                                                                                                                                                     Indels 62;
                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increasing
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 215
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RESULT
AAE01892
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                                                                                                                         17-NOV-1999;
17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                         Transcription factor; biochemical characteristic; controlling element; structural characteristic; developmental characteristic; gene therapy; agricultural biotechnology; plant trait modification.
       Pilgrim
               Creelman
                                                                                                                                                                          25-MAY-2001.
                                                                                                                                                                                           WO200136597-A1
                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                             31-JUL-2001
                                                                                                                                                                                                                                                                                                                                              AAE01892 standard; Protein; 587
                                                                                                  (MEND-) MENDEL BIOTECHNOLOGY INC
(CREE/) CREELMAN R.
                                                                                                                                                          14-NOV-2000; 2000WO-US31344
                                                                                                                                                                                                                                                                                                                              AAE01892;
                                                       HEAR/) HEARD J.
SAMA/) SAMAHA R.
                                                                       ADAM/) ADAM L.
RIEC/) RIECHMANN J L.
                                                                                         YUGG/)
                                                                                                                                                                                                                                                                                                                                                                                      551 nsgqgyrveesngclmlgwhtrplittsawkls
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGDGYKVEEKEGCLTLGWHTRPLIATSAWRLA 621
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                                                                                                                                                                                                                                                                                                                                                                                                                              MSEVYLGRQICNVVACEGAERTERHETLGQWRNRLGNAGFETVHLGSNAYKQASTLLALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALARRVFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         engvrlvhalmacaeaiqqnnltlaealvkqigclavsqagamrkvatyfaealarriyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MQWPALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKLAQFAHTIRVDFQYRGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILGRIM M.
PINEDA O.
       Z
                               JIANG
                                                                                                 CREELMAN
              ₽,
                                                                                         G.
      Pineda
                                                                                                                         99US-0166228.
2000US-0197899.
2000US-0227439.
                                                                                                                                                                                                                                                                                            thaliana
              Yu G,
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                   Location/Qualifiers 323..339
                                                                                                                                                                                                           /label-
       Ó
              Adam L,
                                                                                                                                                                                                                                                                                            transcription factor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC G307. The transcription factor is used for altering a plant's cC biochemical characteristics. The transcription factor may be used to CC alter the structure and developmental characteristics of plants such as CC soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, CC alfalfa, sugár cane, turf, banana, blackberry, blueberry, strawberry, cc raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, CC grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers, CC pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, crosaceous fruits and/or vegetable brassicas. Transcription factors are key controlling elements of biological pathways and altering expression clevels of 1 or more transcription factors can change entire biological pathways in an organism. Therefore manipulating transcription factor CC levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits. Transcription factor CDNA is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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N-PSDB; AAD05776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn, potato and cotton plants -
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                                                                                                                                              1--sppqnqidhclsdtlqmhfyetcpylkfahftanqaileafegkkrvhvidfsmnqg
                                                                                                                                                                                                                                                                                                                                                                           SVRDPKRMRTGGSSTS--SSSSSSSIGGGARSSVVEAAPPVAAAAANATPALPVVVVDTQ 228
                   MSEVYLGRQICNVVACEGAERTERHETLGQWRNRLGNAGFETVHLGSNAYKQASTLLALF 588
                                                                                                                                                                                                                                                MOWPALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKLAQFAHTIRVDFQYRGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLPPAPQLNASTSSTVTGSGGYFDLPPSVD---SSSSIYALRPIPSPAGATAPA-DLSAD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mkrdhhqfqgrlsnhgtssssssiskdkmmmvkkeedgggnmddellavlgykvrssema 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKREYQDAGG----SGGGGGGGMGSSEDKMMV--SAAAGEGEEVDELLAALGYKVRASDMA 54
                                                                                                                                                                                                                             lqwpalmqalalreggpptfrltgigppapdnsdhlhevgcklaqlaeaihvefeyrgfv
                                                                                                                                                                                                                                                                                                                                           FRPQPDSSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEAFAGCRRVHVVDFGIKQG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                        snnqnkrlkscsspdsmvtststgtqiggvigttvttttttttaaaestrs--vilvdsq
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msevylgkqicnlvacegpdrverhetlsqwgnrfgssglapahlgsnafkqasmllsvf
                                                                                                                TVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEGGSSGGGPSEVSSGAAAAPAAAGTDQV 528
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Pred. No. 4.7e-119;
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22 EDKMMYSAAAGEGEEVDELLAALGYKYRASDMADVAQKLEQLEMAMGMGGVGAGAAPDDS 81

dkktmmmneeddgngmdellavlgykvrssemadvaqkleqlevmm----snvqedd- 63

Matches

Similarity

49.9%; Score 1594; DB 18; 54.3%; Pred. No. 1.1e-117;

Length Indels

71; Mismatches 106;

102;

Gaps

11;

Conservative

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RESULT
AAW30792
ID AAW3
XX AAW3
XX AAW3
XX ACA
ACC ACA
DE ACA
DE ACA
XX Gibb
KW Gibb
KW Gibb
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                                                                                                        produce tall or dwarf plants, particularly the latter for increased resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the vegetative state until treated with GA, useful to inhibit bolting in spinach and lettuce. GAI can be used to raise specific antibodies for identifying homologous proteins or genes in other species. gai fragments can also be used as probes or primers to identify and clone related sequences, or in the preparation of antisense or sense expression regulating (co-suppressing) sequences. Rice plants that express GAI may be resistant to Bakane disease. Manipulation of gai and GAI makes it possible to tailor the degree of dwarfism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibberellin insensitivity; gai; plant growth inhibition; dwarf phenotype; lodging resistance; increased yield; flowering regulation; bolting inhibition; spinach; lettuce; antibody; identification; probe; primer; antisense; sense; expression regulation; co-suppression; rice; Bakane disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the Arabidopsis thaliana gibberellin insensitivity (gai) gene product (GAI), the expression of which insensitivity (gai) gene product (GAI), the expression of which inhibits plant growth. However the inhibition is antagonised by gibberellin (GA), while gai expression confers a dwarf phenotypy gibberellin (GA), while gai expression confers a dwarf phenotypy that is insensitive to GA. Manipulating gai and GAI expression or that is insensitive to GA. Manipulating gai and GAI expression or that is insensitive to GA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding gibberellin inhibitor GAI and related antisense sequences - used to create tall, or particularly, plants, especially crops such as maize, rice and wheat
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 4; 76pp; English.
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                                                                             GA sensitivity to particular crops or situations
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on assay; genetic mapping; gene expression control; promot sequence.  thaliana.  2.  2.  2.  2000EP-0301439.  ; 99US-0121825.  99US-0125788.  99US-0125788.  99US-0126264.  99US-0127462.  ; 99US-0128234.  ; 99US-0128234.	tsawkis 530 standard; Protein; 533 AA. 00 (first entry) is thaliana protein fragment SEQ ID NO: 4	AVNSVFEMH::	FATHLATDTVHYNPTDLSSWVESMLSELNAPPPPLPPAQLNASTSSTVTGSGGYFDLPP 141 :   :   :   :  :  :  :  :  :  :  :  :  :
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9908-0160815.
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                                                      ----vpsgqdkvmsevylgkqicnvvacdgpdrv
                                                                                                                                                                                                                                                                                                    Indels 102;
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AAE02545
factors which may be used to modify phenotype associated with a plant's consumer sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the cDNAs and proteins of the invention are useful for modifying the growth and comparition, starch and sucrose synthesis, glyoxylate metabolism, response, wounding response, cell cycle regulation, pigmentation, corresponse, wounding response, cell cycle regulation, pigmentation, corresponse, wounding response, cell cycle regulation, pigmentation, corresponse, and senescence of plants and for modifying sink-source correlationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental correction, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, conffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, melon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant transcription factor; phenotype; sugar sensing characteristic; transgenic plant; plant yield; growth; germination; photosynthesis; glyoxylate metabolism; respiration; pathogen response; wounding response; cell cycle regulation; pigmentation; flowering; senescence; physiology;
                                                                                                                                                                                                                                                                         Claim 4; Page 74-76; 151pp; English.
                                                                                                                                                                                                                                                                                                     Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasin yield, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-335977/35.
N-PSDB; AAD06646.
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17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439
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(HEAR/)
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HEARD J.
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ADAM L.
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YU G.
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Best Local (
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                      Arabidopsis thaliana
                                           agricultural
                                                      Transcription factor; biochemical characteristic; structural characteristic; developmental character
                                                                                       Arabidopsis thaliana transcription
                                                                                                             31-JUL-2001
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                                                                                                                                                         standard; Protein;
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                                            biotechnology;
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                                                      hemical characteristic; controlling developmental characteristic; gene
                                            plant trait modification
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2.2e-117;
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Key

Location/Qualifiers

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Query Match
Best Local Similarity
Matches 331; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                       used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. Transcription factors are key controlling elements of biological pathways and altering expression levels of 1 or more transcription factors can change entire biological pathways in an organism. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits. Transcription factor cDNA is a controlled to the controlled
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17-APR-2000;
22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 114-115; 127pp; English.
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                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn,
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a O, Jiang
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05-MAR-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                     Arabidopsis thaliana protein fragment SEQ ID NO: 47611.
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                                                               The present sequence is given in a specification relating to the CC structure and function of a regulatory gene, SCARECROW (SCR).

CC SCARECROW-like (SCL) genes encoding proteins containing an amino acid CC sequence similar to the sequence of MOTIF III (VHIID) of Arabidopsis SCR protein are disclosed. SCR and SCL genes are useful for producing CC transgenic plants whose cell division is modified and root and/or stem CC development and gravitropism of stem or hypocotyl is altered. Cell CC division is increased or decreased in roots resulting in thicker or CC thinner root development. The transgenic plants are useful for expressing CC a gene of interest encoding a gene product that confers herbicide, salt, CC pathogen or insect resistance in root or embryos and genes encoding CC confers less susceptibility to lodging in the transgenic plants than a CC wild-type plant. SCR gene sequences are also useful as molecular markers CC for a quantitative trait e.g. root or gravitropism trait in molecular for property of the property of the content of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scarecrow gene useful for producing transgenic plants expressing genes whose product increases starch, lignin or cellulose biosynthesis and confers herbicide, pathogen or insect resistance -
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                                                                                                                                                                                                                                                                                                                       protein; BZH gene; transcription factor; gibberellin; morphogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||||||:|:
|| pliatsawkls 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 AA
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Pred. No. 2.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   morphogenesis and plant development. The mutant GRAS protein is used to produce dwarf plants, specifically crucifers. Dwarf plants may be sown earlier (increasing nitrate accumulation without risking excessive stem growth during winter), and have better resistance to cold and lodging. They are also easier to harvest and allow for better
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a wild type plant protein of the GRAS family. The specification describes a mutant allele of the BZH gene, which contains a G1695A mutation resulting in the mutation E546K in the protein. GRAS proteins are transcription factors implicated in regulation of the response to gibberellins and thus in control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             produce dwarf transgenic plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 PPPLPPA-----PQLNASTSSTVTGSGGYFDLPP-----SVDSSSSIYA 151
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                                          AQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGEEDPNEEPEVIAVNSVFEMHRLLAQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MADVAQKLEQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mkrdlhqfqgpnhgtsiagsstsspavfgkdkmmmv----keeeddellgvlgykvrsse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKREYQDAGGSGGGGGGGGGSS------EDKMMVSAAAGEGEEVDELLAALGYKVRASD
               HLGSNAYKQASTLLALFAGGDGYKVEEKEGCLTLGWHTRPLIATSAWRLA
                                                                                                  glekvfgvvkqlkpvlftvveqesnhngpvfldrfteslhyystlfdsleg
                                                                                                                                                                                                                                                   FAGCRRVHVVDFGIKQGMQWPALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKL
                                                                                                                                                                                                                                                                                                           RKVAAYFGEALARRVFRFRPQPDSSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEA
                                                                                                                                                                                                                                                                                                                                                      AAANATPALPVVVVDTQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ppaattgsnalnpeinnnnnsfftggdlkaipgnavcrrsnqfafavdsssn-kr
                                                                                                                                                            aqlaeaihvefeyrgfvansladldasml----elrps-eteavavnsvfelhkllgrtg
                                                                                                                                                                                                                      fegkkrvhvidfsmngglqwpalmqalalreggppsfrltgigppaadnsdhlhevgckl
                                                                                                                                                                                                                                                                             rkvatyfaealarriyrl--sppqtqidhslsdtlqmhfyetcpylkfahftanqailea
                                                                                                                                                                                                                                                                                                                                                                                               lkpsssp-----dsm-----vtspspagvigttvttvtes----
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                                                                                                                                                                                                                                                                                                                                      -----trplilvdsqdngvrlvhalmacaeavqssnltlaealvkqigflavsqagam
337;
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51.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1572; DB 22;
Pred. No. 6.6e-116;
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RESULT 14
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PN WO2-AUG
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Best Local
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plant development;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mutant nucleic acid encoding modified GRAS produce dwarf transgenic plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renard M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2000;
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DB; AAF25481.
  AAANATPALPVVVVDTQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAM
                                                                                                                                                            ----ppaattgsnalnpeinnnnnsfftggdlkaipgnavcrrsnqfafavdsssn-kr 161
                                                                                                                                                                                                                                                                                                     MADVAQKLEQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAP
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Pred. No. 1.4e-115;
1; Mismatches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; transgenic plant; cell division; molecular marker; herbicide resistant resistance; pathogen resistance; insect resistance.
The present sequence is given in a specification relating to the structure and function of a regulatory gene, SCARECROW (SCR). SCARECROW-like (SCI) genes encoding proteins containing an amino acid sequence similar to the sequence of MOTIF III (VHIID) of Arabidopsis: protein are disclosed. SCR and SCL genes are useful for producing transgenic plants whose cell division is modified and root and/or stendevelopment and gravitropism of stem or hypocotyl is altered. Cell
                                                                                                                                                                                                                                                                  Scarecrow gene useful for producing transgenic plants expressing whose product increases starch, lignin or cellulose biosynthesis confers herbicide, pathogen or insect resistance -
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                                                                                                                                                                                                                       Claim
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	DB 1; 10; hes	THE NUCLEAR AMILY AND A OWER, SUITE OWER #1.2	rs	US-08-602-999A-448 US-08-926-258-2 US-09-120-053-2 US-09-138-212-2 US-09-041-886-29 US-08-764-870-7 US-08-980-115-7 US-09-041-886-29 US-07-952-800-2 US-07-952-800-2 US-09-041-886-30 US-08-246-982A-16 US-08-246-982A-16 US-08-246-982A-16 US-08-453-265-16
	Length 1; Ind	UT NO		
	<u>e</u>	CLONE		Sequence
	0;	THEREOF		
	Gaps	,		448, Appli 2, Appli 2, Appli 28, Appli 7, Appli 7, Appli 29, Appli 20, Appli 31, Appli 31, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 17, Appli 18, Appli 19, Appli 19, Appli 11, Appli 11, Appli 11, Appli 12, Appli 13, Appli 142, Appli 15, Appli
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US-09-126-980-2
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                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09126980 Patent No. 6270956
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                                                                         APPLICANT: Jones, Katherine
APPLICANT: Wei, Ping
APPLICANT: Wei, Ping
APPLICANT: Garber, Mitchell
APPLICANT: Garber, Mitchell
APPLICANT: Fang, Shi-Min
TITLE OF INVENTION: A TRANSCRIPTIONAL COACTIVATOR THAT
TITLE OF INVENTION: INTERACTS WITH TAT PROTEZIN AND REGULATES ITS
TITLE OF INVENTION: BINDING TO TAR RNA, METHODS FOR MODULATING TAT
TITLE OF INVENTION: TRANSACTIVATION, AND USES THEREFOR
FILE REFERENCE: SALK2231
CURRENT APPLICATION NUMBER: US/09/126,980
CURRENT FILING DATE: 1998-07-30
CURRENT FILING DATE: 1998-07-30
CURRENT FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/069,341
EARLIER FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 3477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia Bennett
STREET: PO Box 37428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Mouse Model TITLE OF INVENTION: Related DNA NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hayden, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: PO Box 37428
CITY: Raleigh
STATE: No. 5849995th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 27627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 APPPPPPPPPQ 39
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les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 APPPPLPPAPQ 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3118 amino acids
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Nasir, Jamal
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/457,273B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for Huntington's Disease and Sequences
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; SEQ ID NO 2
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-476-482-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Homo sapiens US-09-126-980-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
""" B; Conserv
; ORGANISM: Homo sapien US-08-769-745-31
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US-08-769-745-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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Best Local Similarity
""" Best Local Similarity
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LENGTH: 726
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                               SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/08769745 Patent No. 5955259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09476482 Patent No. 6284456
                                                                                                                                          APPLICANT: Holmes, Todd C.
APPLICANT: Levitan, Irwin B.
APPLICANT: Levitan, Irwin B.
APPLICANT: Brandeis University
TITLE OF INVENTION: Mechanism for the Regulation of Ion
TITLE OF INVENTION: Channel Activity
FILE REFERENCE: BRU96-02
CURRENT APPLICATION NUMBER: US/08/769,745
CURRENT FILING DATE: 1996-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jones, Katherine A.
APPLICANT: Well Ping
APPLICANT: Well Ping
APPLICANT: Well Ping
APPLICANT: Garber, Mitchell
APPLICANT: Fang, Shi-Min
TITLE OF INVENTION: A TRANSCRIPTIONAL COACTIVATOR THAT
TITLE OF INVENTION: INTERACTS WITH TAT PROTEIN AND REGULATES ITS BINDING TO TAR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE OF INVENTION: THEREFOR
FILE OF INVENTION UNMBER: US/09/476,482
CURRENT APPLICATION NUMBER: US/09/476,482
CURRENT FILING DATE: 1999-12-30
EARLIER APPLICATION NUMBER: 09/126,980
EARLIER APPLICATION NUMBER: 1998-07-30
RUMBER OF SEQ ID NOS: 19
COURTENDED: Featers of First Sep For Service Version A. O.
                                                                                                     NUMBER OF SEQ ID NOS: 41 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                         LENGTH: 15
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 717 PPPPLPPLPK 726
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Pred. No. 27;
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; MOLECULE TYPE: protein US-08-810-453-2
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Best Local Similarity
Best Formula (Conserv)
                                                                                                                                                           RESULT 7
US-08-815-190A-2
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US-08-810-453-2
           GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
APPLICANT: Vasquez, William P.
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: Fas Ligand Fus
TITLE OF INVENTION: Uses
TITLE OF SEQUENCES: 17
                                                                                                                              Sequence 2, Application US/08815190A Patent No. 6046310
                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conser
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                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Walsh, Kenneth
TITLE OF INVENTION: FAS LIGAND COMPOSITIONS FOR TREATMENT OF
TITLE OF INVENTION: PROLIFERATIVE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                 50 PPPPLPPPP 58
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                   PPPPLPPAP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617)720-2441
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                                              Fas Ligand Fusion Proteins and
                                                                                                                                                                                                                                                                                                             68.4%;
88.9%;
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                                                                                                                                                                                                                                                                                                                            Length 281;
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                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
SEQ ID NO 25
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,190A

FILING DATE: 11-MAR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/614,584

FILING DATE: 13-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFEDENCE /OCCETT NUMBER: 36,429

REFEDENCE /OCCETT NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/09290640 Patent No. 6204055
                                                                      Matches
                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 0118
REGISTRATION NUMBER: 0118
REFERENCE/DOCKET NUMBER: 0118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEFAX: 7-0-10 NO: 2:
                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 576-031
                                                                                                                                                                             LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 ddd7ddd 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
50 PPPPLPPPP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PPPPLPPAP 12
                                  4 PPPPLPPAP 12
                                                                      Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 amino acids
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                       68.4%;
                                                                    Score 52; DB Pred. No. 15; O; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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RESULT

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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-479-524-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application PC/TUS9500362 GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Matches 8; Conservative
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EARLIER APPLICATION NUMBER: US 09/170,948
EARLIER FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: WordPerfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: US 60/062,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/479,524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barbera-Guillem, Emilio
TITLE OF INVENTION: Polynucleotides For Inhibiting Metastasis And Tumor Cell Growth
FILE REFERENCE: B-37
                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q ID NO 3
LENGTH: 281
                                                                                                                                                                       APPLICATION NUMBER: US 08/179,138
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,559
FILING DATE: 01-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft World, Version 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: US 08/179,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                           NAME: ADJUSTED 17 NAME: 32,1/
REFERENCE/DOCKET NUMBER: 7
REFERENCE/COCKET NUMBER: 7
REFERENCE/COCKET NUMBER: 7
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/00362 FILING DATE: 06-JAN-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 PPPPLPPPP 58
                    TOPOLOGY:
                                                                                                                                NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98101
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                                                       ENGTH:
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                                  amino acids
TYPE: protein
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51 University Street
                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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88.9%;
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Pred. No.
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US-08-545-196B-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6080577 GENERAL INFORMATION:
                                                                                                                                                    Sequence 3, Application US/09028327 Patent No. 6130064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08545196B Patent No. 6080577
                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 205-8050 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/545
FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
                                                               APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: HUMAN SMN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MELKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                          214 PPPPLPPPP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: ami
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ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                          Local Similarity 88.
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               ADDRESSEE:
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amino acid
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E: Incyte Pharmaceuticals, Inc
3174 Porter Dr.
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88.9%;
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 Mismatches

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Pred. No. 15;
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette

CITY: Palo Alto

CA

COUNTRY:

USA

94304

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RESULT 13
US-09-179-558-66
; Sequence 66, Application US/09179558
; Patent No. 6180612
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Best Local Similarity
""" 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE:
US-09-028-327-3
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/179,59
FILING DATE: 27-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
                                                                                                   COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: TARGETING DNA METABOLIC PROCESSES USING TITLE OF INVENTION: AMINOGLYCOSIDE DERIVATIVES
                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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LIBRARY: GELL
ONE: 1857114
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                                                                                                                                                                               STATE:
                                                                                                                                                                                           STREET: 1155 Av
CITY: New York
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                              Hockensmith, Joel W. Muthuswami, Rohini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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88.9%;
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                   US/09/179,558
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Pred. No. 15;
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US-07-945-283-2
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Best Local Similarity
"hes 8; Conserv
                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945,283
FILING DATE: 1920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07945283 Patent No. 5352596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                INFORMATION FOR SEQ ID NO: 2:
TOPOLOGY: li
MOLECULE TYPE:
17-945-283-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U.S. FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION: NAME: COTUZZI, LAULTA A REGISTRATION NUMBER: 30,
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1958 amino aci
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: U.S. FILING DATE: 15-APR-1998 PRIOR APPLICATION DATA:
                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cheung, Andrew K. APPLICANT: Wesley, Ronald D.
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 61604
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STRANDEDNESS: si
                                                                                                                                                                 NAME: Ribando, Curtis P
REGISTRATION NUMBER: 279
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Pred. No. 16;
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COMPUTER READABLE FORM:

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COMPUTER: COMPUTER: COMPUTEN: GOMPATIBLE
COMPUTER: F10ppy disk
COMPUTER: STEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
FILLING DATE: 19-OCT-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 2121-110P
REFERENCE/DOCKET NUMBER: 2121-110P
REFERENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
FELEFAX: (703) 205-8000
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: brokens
MOLECULE TYPE: protein
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; Sequence 63, Application US/08545196B
; Patent No. 6080577
; Patent No. 6080577
; GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
; APPLICANT: MUNNICH, ARNOLD
; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
; CORRESPONDENCES: 65
; CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
; STREET: PO BOX 747
Search completed: January 22, 2002, 16:24:20 Job time: 40 sec
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Matches 8; Conserv
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ZIP: 22040-0747
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CITY: FALLS CHURCH
STATE: VA
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000
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homeobox protein -	immediate-early pr	hypothetical prote	acyl-CoA oxidase h	hypothetical prote	probable cytoskele	probable secretory	high molecular mas	transcription fact	probable protein p	serine/threonine p	scarecrow-like pro	Scl1 protein [impo	scarecrow-like pro	scarecrow-like pro	hypothetical prote

## ALIGNMENTS

C;Genetics: A;Gene: At2g01570 hypothetical protein At2g01570 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001 C;Accession: D84426 R;Lin, X.; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999 Ω 밁 A;Molecule type: DNA A;Residues: 1-587 <STO> A;Cross-references: GB:AE002093; NID:g3785986; PIDN:AAC67333.1; GSPDB:GN00139 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: D84426 A;Status: preliminary Ş δõ 밁 δõ 밁 Ş В В Qy Ş Query Match 50.3 Best Local Similarity 53.6 Matches 339; Conservative 115 111 61 1 MKRDHHQFQGRLSNHGTSSSSSSISKDKMMMVKKEEDGGGNMDDELLAVLGYKVRSSEMA 60 1 MKREYQDAGG----SGGGGGGMGSSEDKMMV--SAAAGEGEEVDELLAALGYKVRASDMA EAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALARRVFR 288 SVRDPKRMRTGGSSTS--SSSSSSSSLGGGARSSVVEAAPPVAAAANATPALPVVVVDTQ PLPPAPQLNASTSSTVTGSGGYFDLPPSVD---SSSSIYALRPIPSPAGATAPA-DLSAD 170 EVALKLEQLETMM------SNVQEDGLSHLATDTVHYNPSELYSWLDNMLSELN--PP DVAQKLEQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPP 114 SNNQNKRLKSCSSPDSMVTSTSTGTQIGGVIGTTVTTTTTTTTAAGESTRS--VILVDSQ PLP------ASSNGLDPVLPSPEICGFPASDYDLKVIPGNAIYQFPAIDSSSS 157 50.3%; Score 1608; DB 2; 53.6%; Pred. No. 3.1e-92; ative 82; Mismatches 150; Length 587; Indels 62; Gaps 408 348 215 228 54 275 13;

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protein F10B6.34 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: H86282
C.H.D. C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
A.;Authors: Salzberg, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.;Accession: H86282
A.;Status: ore limitory
A.;Status: ore limitory
A.;Status: ore limitory
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A; Residues: 1-533 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005172; NID:g8778219; PIDN:AAF79228.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 332; Conserv
                         311 YESCPYLKFAHFTANQAILEAFAGCRRVHVVDFGIKQGMQWPALLQALALRPGGPPSFRL
                                                                                                                                                                                                                                                                                                                                                      142 SVDSSSSIYALRPIPSPAGATAPADLSADSVRDPKRMRTGGSSTSSSSSSSSSSSLGGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 DKKTMMMNEEDDGNGMDELLAVLGYKVRSSEMADVAQKLEQLEVMM-----SNVQEDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGDGYKVEEKEGCLTLGWHTRPLIATSAWRLA 621
| ||:|| || || |||||| |||| ||:|:
NSGQGYRVEESNGCLMLGWHTRPLITTSAWKLS 583
                                                                                                                              FATHLATDTVHYNPTDLSSWVESMLSELNAPPPPLPPAPQLNASTSSTVTGSGGYFDLPP
: |||:||||| :| :|::|||::|| |
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YETCPYLKFAHFTANQAILEAFQGKKRYHYIDFSMSQGLQWPALMQALALRPGGPPVFRL
                                                                                                  TVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRL--SPSQSPIDHSLSDTLQMHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSEVYLGRQICNVVACEGAERTERHETLGQWRNRLGNAGFETVHLGSNAYKQASTLLALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATLADLEPFMLQPEGEEDPNEEPEVIAVNSVFEMHRLLAQPGALEKVLGTVRAVRPRIV 468
                                                                                                                                                                                                    YTTNKRLKCSNGVVE-----TTTATAESTRHVVLVDSQENGVRLVHALLACAEAVQKENL
                                                                                                                                                                                                                                                                                                       ---SSNAEYDLKAIP------GDAIL-----NQFAIDSASSSNQGGGGDT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSEVYLGKQICNLVACEGPDRVERHETLSQWGNRFGSSGLAPAHLGSNAFKQASMLLSVF
                                                                                                                                                                                                                            -----arssvveaappvaaaanatpalpvvvvdtqeagirlvhallacaeavqqenl
                                                                                                                                                                                                                                                                                                                                                                                                         -LSQLATETVHYNPAELYTWLDSMLTDLNPP-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.9%; Score 1594; DB 2; Length 533; 54.3%; Pred. No. 2e-91; tive 71; Mismatches 106; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference and analysis of chromosome 1 of the plant Arabidopsis.

A;Recession: G96688
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A;Map position: 1
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A; Residues: 1-511 <STO>
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Best Local S
Matches 324
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                            159
                                                   241 CAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALARRVFRFRPQPDSSLLDA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 324; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKREYQDAGGSGGGGGGGGGSSEDKMMVSAAAGEGEEVDELLAALGYKVRASDMADVAQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKREHNHRESSAGEGG--SSSMTTVIKEEAAG----VDELLVVLGYKVRSSDMADVAHKL
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                                                                                                                                                                           GGSSTSSSSSSSSSIGGGARSSVVEAAPPVAAAANATPALPVVVVDTQEAGIRLVHALLA 240
                                                                                                                                                                                                                                                                          QLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRDPKRMRT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.3%; Score 1511.5; DB 2; 52.3%; Pred. No. 2.5e-86; tive 65; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- VPSGQDKVMSEVYLGKQICNVVACDGPDRV
                                                                                                                         VVVLDSQETGVRLVHALLA
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A;Cross-references: EMBL:AL391150
A;Experimental source: cultivar Columbia; BAC C;Genetics:
A;Map position: 5
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submitted to the Protein Sequence
A:Reference number: 225394
A:Accession: T51475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGA-like protein - Arabidopsis thaliana
N;Alternate names: protein Knd6_60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000
C;Accession: T51475
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A;Molecule type: DNA
A;Residues: 1-523 <SAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCLLLGWQTRPLIATSAWRI 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCLTLGWHTRPLIATSAWRL 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFLDRFTESLHYYSSLFDSLE----GPPSQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPEGEEDPNEEPEVIAVNSVFEMHRLLAQPGALEKVLGTVRAVRPRIVTVVEQEANHNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPGGPPSFRLTGVGPPQPDETDALQQVGWKLAQFAHTIRVDFQYRGLVAATLADLEPFML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVRASDMADVAQKLEQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESML 106
                                                                                                                                                                                                                                                                                                                                                        MKREYQDA------GGSGGGGGGGGGGGSSEDKMMVSAAAGEGEEVDELLAALGY 46
               FRERPQPDSSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEAFAGCRRVHVVDFGIK 346
                                                             TQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALARRV
                                                                                                                               CCSSNSNSNKRIRLGPWCDSVTSESTRS-------
                                                                                                                                                                                                                           SELNAPPPPLPPAPQLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPAD 166
                                                                                                                                                                                                                                                            KVRSSDMADVAQKLEQLEMVL-----SNDIASSSNAFNDTVHYNPSDLSGWAQSML
                                                                                                                                                                                                                                                                                                                           MKRSHQETSVEEEAPSMVEKLENGCGGGG-----DDNM-----DEFLAVLGY 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPNGPPDFRLTGIGYSLTD----IQEVGWKLGQLASTIGVNFEFKSIALNNLSDLKPEML
YRI---HPSAAAIDPSFEEILQMNFYDSCPYLKFAHFTANQAILEAVTTSRVVHVIDLGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFSDTLQIHFYESCPYLKFAHFTANQAILEVFATAEKVHVIDLGLNHGLQWPALIQALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DIRPGLESVAVNSVFELHRLLAHPGSIDKFLSTIKSIRPDIMTVVEQEANHNGT
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                        45.4%; Score 1450.5; DB 2;
49.3%; Pred. No. 1.5e-82;
tive 76; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T.; Kato,
Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-Aug-2000 #text_change 18-Aug-2000
                                                                                                                                                                                             DLDP----NRICDLRPI----TDDDE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T.; Asamizu, E.; Kotani, H.; Tabata, August 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone K3M16
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267
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T47581
T47581 - Arabidopsis thaliana
SCARECROW1 - Arabidopsis thaliana
N;Alternate names: protein F24B22.180
N;Alternate names: thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; osubmitted to the Protein Sequence Database, January 2000 A;Reference number: 23016 A;Accession: T47581 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 3
A; Introns: 511/2
A; Note: F24B22.180
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A;Experimental source: cultivar C
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A; Residues: 1-653 <BLO>
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Best Local Sin
Matches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Genetics:
383
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                                                                                                                       AAYFGEALARRVF------RFRPQPDSSLLDAAFADLLHAHFYESCPYLKFAHF 322
                                                                                                                                                                                                                                                          SVRDPKRMRTGGSSTSSSSSSSSSSSSSSSVEAAPPVAAAANATPALPVVVVDTQEA
                                                                                                                                                                                                                                                                                                                                                                                        DDSFATHLATDTVHYNPTDLSSWVESMLSEL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFAGGDGYKVEEKEGCLTLGWHTRPLIATSAWRLA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVTVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEGGSSGGGPSEVSSGAAAAPAAAGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGMQWPALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKLAQFAHTIRVDFQYRG
ALQQVGWKLAQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGEEDPNEEPEVIAVNSVFE 442
                              TANQAIQEAFEKEDSVHIIDLDIMQGLQWPGLFHILASRPGGPPHVRLTGLG----TSME
                                                                                                                                                          LRERKEEIKRQKQDEEGLHLLTLLLQCAEAVSADNLEEANKLLLEISQLSTPYGTSAQRV
                                                                                                                                                                                                                         ----PQQQQQHQQQQQHKPPPPPIQQQERENSSTDAPPQPETVTAT---VPAVQTNTAEA
                                                                                                                                                                                                                                                                                          LLEYRLRSLMLLDPSSSS-------DPSPQTFEPLYQISNNPSP------
                                                                                                                                                                                                                                                                                                                                                        DQDSSSSSASPTV------WVDAIIRDLIHSSTSVSIPQLIQNVRDIIFPCNPNLGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGMQWPALMQALALRPGGPPSFRLTGVG--NPSNREGIQELGWKLAQLAQAIGVEFKFNG
                                                                                             AAYFSEAMSARLLNSCLGIYAALPSRWMPQTHSLKMVSAF----QVFNGISPLVKFSHF
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                         -----STSSTYTGSGGYFDLPPSYDSSSSIYALRPIPSPAGATAPADLSAD 170
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                           ----GIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKV
                                                                                                                                                                                                                                                                                                                                                                                                                       18.9%; Score 604.5; DB 2; 30.0%; Pred. No. 5.3e-30; Live 84; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Columbia; BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518
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                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 131;
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H.; Tallo

Marzia Kin, Dewar,

Alon

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A;Cross-references: E
C;Genetics:
A;Gene: SCARECROW1
A;Introns: 511/2
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C;Accession: T51244
R;d1 Laurenzio, L.; Wysocka-Diller, J.; Malamy, J.E.;
submitted to the EMBL Data Library, July 1996
A;Reference number: Z25338
A;Accession: T51244
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
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A; Residues: 1-653 <DIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALQATGKRLSDFADKLGLPFEFCPL-AEKVGNLDTERLNV-----RKREAVAVH--WL
                  GSSGGGPSEVSSGAAAAPAAAGTDQVMSEVYLGRQICNVVACEGAERTERHETLGQWRNR
                                                          QHSLYDVTGSDAHTLWLLQRLAPKVVTVVEQDLSH-AGSFLGRFVEAIHYYSALFDSL--
                                                                                              MHRLLAQPGALEKVLGTVRAVRPRIVTVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEG 502
                                                                                                                                       ALQATGKRLSDFTDKLGLPFEFCPL-AEKVGNLDTERLNV-----RKREAVAVH--WL
                                                                                                                                                                           ALQQVGWKLAQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGEEDPNEEPEVIAVNSVFE 442
                                                                                                                                                                                                                    TANQAIQEAFEKEDSVHIIDLDIMQGLQWPGLFHILASRPGGPPHVRLTGLG----TSME
                                                                                                                                                                                                                                        TANQAILEAFAGCRRVHVVDEGIKQGMQWPALLQALALRPGGPPSFRLTGVGPPQPDETD
                                                                                                                                                                                                                                                                                                AAYFSEAMSARLLNSCLGIYAALPSRWMPQTHSLKMVSAF----QVFNGISPLVKFSHF
                                                                                                                                                                                                                                                                                                                                       AAYFGEALARRVF------RFRPQPDSSLLDAAFADLLHAHFYESCPYLKFAHF 322
                                                                                                                                                                                                                                                                                                                                                                             LRERKEEIKRQKQDEEGLHLLTLLLQCAEAVSADNLEEANKLLLEISQLSTPYGTSAQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PQQQQQHQQQQQQHKPPPPPIQQQERENSSTDAPPQPETVTAT--VPAVQTNTAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVRDPKRMRTGGSSTSSSSSSSSSSIGGGARSSVVEAAPPVAAAANATPALPVVVVDTQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQDSSSSSASPTV------WVDAIIRDLIHSSTSVSIPQLIQNVRDIIFPCNPNLGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDSFATHLATDTVHYNPTDLSSWVESMLSEL------NAPPPPLPPAPQLNA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MQQCGFKGISLAGNAATQATLLLGMFP-SDGYTLVDDNGTLKLGWKDLSLLTASAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----STSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSAD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: U62798; PIDN: AAB06318.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%; Score 600.5; DB 2; 29.9%; Pred. No. 9.3e-30; tive 84; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                -GIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ERHVVEQQLLSKEIRNVLAVGGPSRSGEVK-FESWREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F11F12.22 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
C;Accession: E95540
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marzia
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719
A;Accession: E95340
A;Status: prelininary
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A;Gene: F11F12.22
A;Map position: 1
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A; Residues: 1-482 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 147; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GGSSTSSSSSSSSLGGGARSSVVEAAPPVAAAANATPALPVVVVDTQEAGIRLVHALLA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALARRVFRFRPQPDSSLLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 GTSSVASSPLQVFSTMSLNRPTLLASSSPFHCLKDLKP-----EERGLYLIHLLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQQCGFKGISLAGNAATQATLLLGMFP-SDGYTLVDDNGTLKLGWKDLSLLTASAW
                                                                                                                                                                               VDLQRVLMMSHGSAAEARENDMSNNNGYSPSGDSASSLPLPSSGRTDSFLNAIWGLSPKV
                                                                                                                                                                                                                                                                                                                                                                                                                  QWPALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKLAQFAHTIRVDFQYRGLVA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNATQTRINNVSEEIHVRRLFFEMFPILKVSYLLTNRAILEAMEGEKMVHVIDLDASEPA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CANHVASGSLQNANAALEQLSHLASPDGDTMQRIAAYFTEALANRILKSWP----GLYKA
    GCGFDGYRIKEESGCAVICWQDRPLYSVSAWR
                                      FAGGDGYKVEEKEGCLTLGWHTRPLIATSAWR 619
                                                                          KVEKMLFGEEIKNIISCEGFERRERHEKLEKWSQRIDLAGFGNVPLSYYAMLQARRLLQ- 447
                                                                                                                                                         MVVTEQDSDHNGSTLMERLLESLYTYAALFDCLE-----
                                                                                                                                                                                                                                                                                                                     RLDCLNVEQLRV-----KTGEALAVSSVLQLHTFLASDDDLMRKNCALRFQNNPSG
                                                                                                                                                                                                                                                                                                                                             -ATLADLEPFMLQPEGEEDPNEEPEVIAVNSVFEMHRLLA-----
                                                                                                                                                                                                                                                                                                                                                                                             OWLALLQAFNSRPEGPPHLRITGV----HHQKEVLEQMAHRLIEEAEKLDIPFQFNPVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GASYGEESE --
                                                                                                   VMSEVYLGRQICNVVACEGAERTERHETLGOWRNRLGNAGFETVHLGSNAYKOASTLLAL 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
    479
                                                                                                                                                                                                                                                                              ----QPGALEKVLGTVRAVRPRI 467
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                                                                                                                                                           ----TKVPRTSQDRI 388
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonsc Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference number: A86141; MUID:21016719

A;Accession: B96542

A;Accession: B96542
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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C;Genetics:
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A; Residues: 1-526 <STO>
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RESULT
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Best Local Similarity
Matches 149; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 DSSSSIYALRPIPSPAGATAPADLSADSVRDPKRMR----TGGSSTSSSSSSSSSLGGGA 199
                                                                                                                                                                             439
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                                                                                                                                                                                                                                                                                                      DLEPFMLQPEGEEDPNEEPEVIAVNSVFEMHRLLAQPGALE----KVLGTVRAVRPRIVT
                                                                                                                         GGDGYKVEEKEGCLTLGWHTRPLIATSAWR 619
                                                                                                                                                                                                                                                                            LVEQEANTNTAPFLPRFVETMNHYLAVFESIDVKLARDHKERIN--
                                                                                                                                                                                                                                                                                                                                                                                EIEKLGVR-----NGEALAVNFPLVLHHMPDESVTVENHRDRLLRLVKHLSPNVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALGARPGGPPNVRITGIDDPRSSFARQGGLELVGQRLGKLAEMCGVPFEFHGAALCCTEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALALRPGGPPSFRLTGVGPPQPD--ETDALQQVGWKLAQFAHTIRVDFQYRG-LVAATLA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPTGPELLTYMHILYEACPYFKFGYESANGAIAEAVKNESFVHIIDFQISQGGQWVSLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALARRVFRFRPQPDSSLLDAAFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSSVVEAAPPVAAAANATPALPVVVVDTQEAGI--------RLVHALLACAEA 244
                                                                                                                                                                             EQHCLAREVVNLIACEGVEREERHEPLGKWRSRFHMAGFKPYPLSS--YVNATIKGLLES
                                                                                                                                                                                                                       SEVYLGRQICNVVACEGAERTERHETLGQWRNRLGNAGFETVHLGSNAYKQASTLLALFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LLHAH-FYESCPYLKFAHFTANQAILEAFAGCRRVHVVDFGIKQGMQWPALLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VENYDLEMTDWLISQLQQMVSVSGEPVQRLGAYMLEGLVARL----ASSGSSIYKALRCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETAMME - - PDVDNSYNNQGGF - - - - - - GQQHGVVSSAMYRSMEMISRGDLKGVLYECAKA
                                                                            YSEKYTLEERDGALYLGWKNQPLITSCAWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.5%; Score 558; DB 2; Length 526, 29.2%; Pred. No. 3e-27; rative 97; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72;
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G84462

probable SCARECROW

gene regulator [imported] - Arabidopsis thaliana

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Rytheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vender, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: D96656
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F16M19.21 [imported] - Arabidopsis thallana C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96656
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A; Map position: 2
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A; Residues: 1-413 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D96656
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C;Genetics:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508 GPSEVSSGAAAAPAAAGTDQVMSEVYLGRQICNVVACEGAERTERHETLGQWRNRLGNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 EALARRYF-----RFRPQPDSSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEA 331
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GB:AE005173; NID:g6598840; PIDN:AAF18695.1; GSPDB:GN00141

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A;Cross-references: (C;Genetics: A;Gene: F16M19.21 A;Map position: 1
                                                                                                                                                                                                           C;Accession: T51242
R;Pysh, L.D.; Wysocka-Diller, J.W.; Camilleri, C.; Bouchez, D.; Benfey, P.N. Plant J. 18, 111-119, 1999
A;Title: The GRAS gene family in Arabidopsis: sequence characterization and A;Reference number: Z25337; MUID:99272994
A;Accession: T51242
                                                                                                A;Cross-references: EMBL:AF067400; PIDN:AAC98090.1
C;Genetics:
A;Gene: Scl1
                                                                                                                                                     A;Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 1-313 <PYS>
                                                                                                                                                                                                                                                                                                                            Scll protein (imported) - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change
  Query Match
Best Local S
Matches 112
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;Gene: F16M19.21
;Map position: 1
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Best Local Similarity
Matches 165; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     632 GGRGGGVTLRWSEQPLYTISAWTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                               11
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                    16.0%;
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  48;
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  Score 512; DB 2;
Pred. No. 1.1e-24;
8; Mismatches 107
                                                                                                                                                                                           from GB/EMBL/DDBC
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    107;
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  34;
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A;Title: The GRAS gene family in Arabidopsis: sequence A;Reference number: Z25337; MUID:99272994
A;Accession: T51236
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-C;Accession: T51236
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A;Molecule type: mRNA
A;Residues: 1-306 <PYS>
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A;Gene: SCL5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 TYAGLTQVWFDPDEVDTLKDQLIHVTSLSGSGFNILVCDGSLALAWHNRPLYVATAWCVT
                                                                                                                                                                                                                                                                                                                                                                                                               10
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                                          EEKEGCLTLGWHTRPLIATSAWR 619
                                                                                                                     QICNVVACEGAERTERHETLGQWRNRLGNAGFETVHLGSNAYKQASTLLALFAGGDGYKV 596
                                                                                                                                                                           TNTAPFLPRFVETMNHYLAVFESIDVKLARDHKERIN----
                                                                                                                                                                                                                                                      R-----NGEALAVNEPLVLHHMPDESVTVENHRDRLLRLVKHLSPNVVTLVEQEAN
                                                                                                                                                                                                                                                                                          QPEGEEDPNEEPEVIAVNSVFEMHRLLAQPGALE----KVLGTVRAVRPRIVTVVEQEAN 476
                                                                                                                                                                                                                                                                                                                                                                                                             LTYMHILYEACPYFKFGYESANGAIAEAVKNESFVHIIDFQISQGGQWVSLIRALGARPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNAGFETVHLGSNAYKQASTLL--ALFAGGDGYKVEEKEGCLTLGWHTRPLIATSAWRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YAHSVGIDFTFQGVCVDQLDRLCDWMLLKP-----IKGEAVAINSILQLHRLLVDPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAHTIRVDFQYRGLVAATLADLEPFM-LQPEGEEDDNEEDEVIAVNSVFEMHRLLAQPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYNHVHIIDFSLMQGLQMPALMDVFSAREGGPPKLRITGIGPNPIGGRDELHEVGIRLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCRRVHVVDFGIKQGMQWPALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKLAQ
                        EERDGALYLGWKNQPLITSCAWR
                                                                                                                                                                                                               HNSGTFLDRFTESLHYYSTMFDSLEGGSSGGGPSEVSSGAAAAPAAAGTDQVMSEVYLGR
                                                                                                                                                                                                                                                                                                                                GPPNVRITGIDDPRSSFARQGGLELVGQRLGKLAEMCGVPFEFHGAALCCTEVEIEKLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPVVPAPIDILLKLVIKINPMIFTVVEHEADHNRPPLLERFTNALFHYATMFDSLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LEKVLGTVRAVRPRIVTVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEGGSS
                                                                                                EVVNLTACEGVEREERHEPLGKWRSRFHMAGFKPYPLSS--YVNATIKGLLESYSEKYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AMHRCTSGRDITDSLTEVYLRGEIFDIVCGEGSARTERHELFGHWRERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.9%;
35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 507; DB 2; Length 306;
; Pred. No. 2.1e-24;
63; M1smatches 113; Indels
                        306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characterization and
                                                                                                                                                                           -----VEQHCLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziall,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719
scarecrow-like protein 1 [imported] - Arabidopsis thaliana (fragment) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000 C;Accession: T51234 R;Pysh, L.D.; Wysocka-1919 Plant J. 18, 111-119, 1999 A;Title: The GRAS gene family in Arabidopsis: sequence characterization and
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A; Residues: 1-593 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AAF87898.1 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: E86347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.b
                                                                                                                                                                                                                                                                                                                                                           406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALARRV-----FRFR----PQPD
                                                                                                                                                                                                                                                                  562 Q-QYCNKYKLKEEMGELHFCWEEKSLIVASAWR 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 SPKESSSADSNSHVSSKEVVSQATPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 STSSSSSSSSIGGGARSSVVEAAPPVAAAANATPALPVVVVDTQEAGIRLVHALLACAE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                               LFAGGDGYKVEEKEGCLTLGWHTRPLIATSAWR 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQALALRPGGPPSFRLTGVGPPQPDETD--ALQQVGWKLAQFAHTIRVDFQYRGLVAATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVTVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEGGSSGGGPSEVSSGAAAAPAAAGTD 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIVSPSTLGCKP------GETLIVNFAFQLHHMPDESVTTVNQRDELLHMVKSLNPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADLEPFML--QPEGEEDPNEEPEVIAVNSVFEMHRL----LAQPGALEKVLGTVRAVRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDERLAAMQVL----FEVCPCFKFGFLAANGAILEAIKGEEEVHIIDFDINQGNQYMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEAFAGCRRVHVVDFGIKQGMQWPAL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVTVVEQDVNTNTSPFFPRFIEAYEYYSAVFESLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRSTAELPGKRPRLRLTGIDDPESVQRSIGGLRIIGLRLEQLAEDNGVSFKFKAMPSKT-
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family in Arabidopsis: sequence characterization and basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.6%; Score 498; DB 2; 29.6%; Pred. No. 1.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 593
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A;Gene:
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A;Reference number: Z25337; MUID:99272994
A;Accession: T51234
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <PYS>
                                                                                                                                                                                                                              R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1336 <ROU>
A;Cross-references: EMBL:AC005315; NID:g3461834; PID:g3461846
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T02736; A84692
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence.
A;Reference number: Z14710
A;Accession: T02736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable SCARECROW gene regulator [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: AF036300; PIDN: AAD24403.1
A;Cross-references: GB:AE0
C;Genetics:
A;Gene: At2g29060; T9I4.14
A;Map position: 2
                                                                                                                        A; Molecule type: DI
A; Residues: 1-1336
                                                                                                                                                                                                         A; Reference number: A84420; A; Accession: A84692
                                                                                                                                                                           A; Status: preliminary
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Matches 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEMGELHFCWEEKSLIVASAWR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVNIVACEGEERIERYEAAGKWRARMMMAGFNPKPMSAKVTNNIQNLIKQ-QYCNKYKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEGEEDPNEEPEVIAVNSVFEMHRL----LAQPGALEKVLGTVRAVRPRIVTVVEQEANH 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRLRLTGIDDPESVQRSIGGLRIIGLRLEQLAEDNGVSFKFKAMPSKT-SIVSPSTLGCK 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSGTFLDRFTESLHYYSTMFDSLEGGSSGGGPSEVSSGAAAAPAAAGTDQVMSEVYLGRQ 537
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31.4%; Pred. No. 1.2e-21;
tive 67; Mismatches 147
                                                                                          NID:g3461846;
                                                                                          PIDN: AAC33232.1;
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                                                                                          GSPDB:GN00139
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A; Introns: 694/2

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                                                                                                                                                                                            572 TREREVLEHYSSLEDMCDTNLTREDPMRV------MFEKEFYGREIMNVVA 616
672 DCHWLLQGWKGRIVYGSSIW 691
                                                601 GC--LTLGWHTRPLIATSAW 618
                                                                                                                               544 CEGAERTERHETLGQWRNRLGNAGFETVHLGSNAYKQASTLLALFAGGDGYKVEE---KE 600
                                                                                                                                                                                                                                                                                                513 -LKEGEFVAVNSLFRFRNLLDETVAVHSPRDTVLKLIRKIKPDVFIPGILSGSYNAPFFV 571
                                                                                                                                                                                                                                                                                                                                      428 PNEEPEVIAVNSVFEMHRLLAQPGAL----EKVLGTVRAVRPRIVTVVEQEANHNSGTFL 483
                                                                                                                                                                                                                                                                                                                                                                                            464 ELPQRGFRPAEGVIETGRRLAKYCQKFNIPFEYNAIAQKWESIKLEDLK------ 512
                                                                                                                                                                                                                                                                                                                                                                                                                             374 GPPQPD--ETDALQQVGWKLAQFAHTIRVDFQYRGLV----AATLADLEPFMLQPEGEED 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 YLKFAHFTANQAI--LEAFAGCRRVHVVDFGIKQGMQWPALLQALALRPGGPPSFRLTGV 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 IROHSSSYGDGTERLAHYFANSLEARLAGIGTQVYTALSSKKTSTSDMLKAYQTYISVCP 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 SPKGEKPEASGNSYTKETPDLRTM------------LVSCAQAVSINDRRTADELLSR 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 ------TPALPVVVVDTQEAGIRLVHALLACAEAVQQENLSAAEALVKQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 EEHLTEERSKKQSAIYVDETDELTDMFDNILIFGEAKEQPYCILNESFPKEPAKASTFSK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 GSSFSGDLVSNMFNDTDL-ALQFKKGMEEASKFLPKSSQLVIDNSVPNRL-TGKKSHWRE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 GSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRD---PKRMRTGGSS---- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 TTTTSSDSQWSFDCLENNRP--SSWLQT------PIPSNFIFQSTSTRASSGNAVF 179
                                                                                                                                                                                                                                             484 DRFTESLHYYSTMFDSLEGGSSGGGPSEVSSGAAAAPAAAGTDQVMSEVYLGRQICNVVA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 FKKIAIIFANHSIMRLASSANAKTIHIIDFGISDGFQWPSLIHRLAWRRGSSCKLRITGI 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 IPLLAASQGGAMRKVAAYFGEALARRVFRFRPQPDSSLLD--AAFADLLHAH--FYESCP 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 APDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPPPLP-----PAPQLNASTSSTVT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 EDK--MMVSAAAGEGEEVDELLAALG--YKVRASDM-ADVAQKLEQLEMAMGMGGVGAGA 76
                                                                                                CEGTERVERPESYKOWOARAMRAGEROIPLEKELVQKLKLMVE----SGYKPKEFDVDQ 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDKPCMFHDALSLQAAE-KSLYEALGEKYPVDDSDQPLTTTTSLAQLVSSPG-GSSYASS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
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Search completed: January 22, 2002, 16:24:46 Job time: 66 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length:
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Match
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3194
1 MKREYQDAGGSGGGGGGMGS.....TLGWHTRPLIATSAWRLAGP
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             GenCore version Copyright (c) 1993 - 2000
                                       Length
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IE18 PRVKA
HXAA MOUSE
IE18 PROUGE
IE18 PROUGE
CRIGAT
CRIGAT
CAPL LONGA
EXY2 SACER
CUT1_MOUSE
SOX4_HUMAN
A180_RAT
CAPL LOROME
AF17_HUMAN
ICP4_HSVEN
BCA1_HUMAN
VIV_ORYSA
MAZ3_SCHCO
CBE_HSVEN
ICP4_HSVEN
ICP4_HSVE
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P33479
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                                                                                                                                                                                                                                                                                                                 4 mus musculu
5 homo sapien
0 rattus norv
0 drosophila
6 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 mus musculu
6 ustilago ma
2 saccharopol
a equine herp
bomo sapien
crattus norv
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crat
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gallus gall
homo sapien
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homo sapien
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			RESULT SOX3.MOUS ID SOX3.1 AC P537 AC P1-0 DT 01-0 DT 18-J DE TRAN GN SOX3 OS Mus   OC Mamm OX NCBI	CCCC4444440000000000000000000000000000
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box. ; Transcription regula POLY-GLY. HMG BOX. POLY-ALA.	yright. It is produced of Bioinformatics and Institute. There are notions as long as its contramoved. Usage agreement (See http://wisb-sib.ch).	25802; Hacker A., Cohen-Tann novic M., Goodfellow P.N ties of Sox-3 with Sry a 5) GLEAR NLY IN THE DEVELOPING CE	PRT; 375 AA.  ed) sequence update) annotation update) ar, Craniata; Vertebrata; a; Sciurognathi; Muridae;	BRN1_HUMAN YK82_MYCTU 7UP2_DROME N121_HUMAN ICP4_HSV11 YAG3_YEAST FSH_DROME YIQ9_YEAST N214_HUMAN CBP_MOUSE MUC2_HUMAN ALIGNMENTS
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Query Match
Best Local Similarity 20.4
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01-JUN-1994 (Rel. 29, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
                                                                                                                                                                        EMBL; X71135; CAA50465.1;
EMBL; X65665; CAA46616.1;
PIR; S21483; S21483.
PIR; S22942; S22942.
                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: CONTAINS 1 HMG BOX.
-!- CAUTION: WAS CALLED SOX-9 BY REF.2.
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MEDLINE-92310993; PubMed-1614875;
Denny P., Swift S., Brand N., Dabhade
"A conserved family of genes related t
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Stevanovic M., Lovell-Badge R., Colli
"SOX3 is an X-linked gene related to
Hum. Mol. Genet. 2:2013-2018(1993).
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Mammalia; Eutheria;
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DOMAIN
         Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
-!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-!- FTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
                                                                                                                                                                                                Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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                                                                                      REVISIONS
                                                                                                            Nucleic Acids Res. 17:4637-4646(1989)
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(Rel. 14, Last sequence unit (Rel. 28, Last annotation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARRLDPRPLGARSPVSSNPNSSSSSTTTVAVEPVARGPEKDEDGLGLAGDGG---APLQR
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AWTYAAALFAPANVAGARLAEAAARPGPAEPAPGLPPLWPEQPGLVVPAPAPAAAG
                                                                                                                 AGEATVEALCARVRAAFAAAQPGRVPRELADACVLACRGVLE--RLLPCPLRLPAPARAP
                                                                                                                                                                            PLPHIGDAMAAQDPLWALPHAVSAVAMSRRYDRTQKTFILQSLRRAYADMAYPGRAADPR
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                                                        AALGPACLEEVTAALLALRDAIPGAGPAERQQAADSVALVARTVAPLVRYSVDGARAREA
                                                                                     --AQPGALEKVLGTVRAVRPRI--VTVVEQEANHNSGTFLDRFTESLHYYS-----
                                                                                                                                                ---ATLADLEPFMLQPEGEEDPNEEPE-----VIAVNSVFEMHRLL-------
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Pred. No. 1;
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P115_CHICK
AC 098917;
DT 15-JUL-1998
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DT 15-JUL-1998
DT 15-JUL-1998
DT 15-JUL-1998
DT 20-AUG-2001
GN 15-JUL-1998
DT 20-AUG-2001
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GN GAILUS 9411
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15-JUL-1998 (Rel. 36, C
15-JUL-1998 (Rel. 36, C
20-AUG-2001 (Rel. 40, I
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"Complete sequence and expression of a
115-kDa melanosomal matrix protein.";
Pigment Cell Res. 4:41-47(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000601; I
Pfam; PF00801; PKD; 1
SMART; SM00089; PKD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WHITE LEGHORN; TISSUE-Retinal pigment epithelium, MEDLINE-88311098; PubMed=3409326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=WHITE LEGHORN; TISSUE=Retinal pigment MEDLINE=92020667; PubMed=1924173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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SIMILARITY: BELONGS TO THE PMEL-17/NMB
SIMILARITY: CONTAINS 1 PKD DOMAIN.
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TISSUE SPECIFICITY: SPECIFIC TO PIGMENTED EPITHELIAL CELLS
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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SEQUENCE OF 301-383 FROM N.A. SEQUENCE OF 301-383; PubMed=2573064; Shen W.-F., Largman C., Lowney P., Hauser C.A., Simonitch T.A., Hack F "Lineage-restricted expression of F hematopoietic cell lines.";
                                                                                                                                                                                                         SEQUENCE
Bradshaw
                                                                                                                                                                                                                                                                                                                                                    Lawrence H.J., Largman C.;
"A human Hox 1 homeobox gene exhibits myeloid-specific expression alternative transcripts in human hematopoietic cells.";
Nucleic Acids Res. 19:3443-3449(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HXAA_HUMAN STANDARD; PRT; 393 AA p31260; Q15949; Q43605; Q43370; Q1-JUL-1993 (Rel. 26, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40
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22.4%;
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                         F.M., Lawrence H.J.;
homeobox-containing genes
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(HOX-1.8) (PL).
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                                                Corral J.C., Detmer K., F.M., Lawrence H.J.;
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RA Castronovo V., Kusaka M., Chariot A., Gielen J., Sobel M.;

"Homeobox genes: potential candidates for the transcriptional control
at of the transformed and invasive phenotype.";

Blochem. Pharmacol. 47:137-143(1994).

Liochem. Pharmacol. 47:137-143(1994).

Developmental regulatory system that provides cells with
specific positional identities on the auterior-posterior axis.

Specific positional identities on the auterior-posterior axis.

Specific positional identities on the auterior-posterior axis.

Specific positional sequence 5'-aa[at]Tittattac-3'.

Subscellular location: NUCLEAR.

Subscellular location: NUCLEAR.

C-1- SUBSCELLULAR LOCATION: NUCLEAR.

C-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PL1 (SHOWN HERE) AND 2/PL2;

ARE PRODUCED BY ALTERNATIVE SPLICING.

C-1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A NUMBER OF FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M30599; AAA36006.1; -.
EMBL; S69027; AAD14030.1; -.
EMBL; S69029; AAD14031.1; -.
PIR; S14930; S14930.
PIR; S26402; S26402.
PIR; A34425; A34425.
PIS; P02833; ISAN.
    CONFLICT
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CONFLICT
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"The human HOX gene family.";
Nucleic Acids Res. 17:10385-10402(1989).
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PROSITE; PS50071; HOMEOBOX_2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
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InterPro; IPR001356; Homeobox.
InterPro; IPR001976; Wilms_tumour.
Pfam; PF00046; homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T01713; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X58430; CAB86198.1; ALT_|
AF040714; AAB96917.1; -.
AC004080; AAB97941.1; -.
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                                                                                                                                                                                                                                                                                                                    PR00024; HOMEOBOX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98876; PubMed=2574852;
, D'Esposito M., Faiella A.,
Stornaiuolo A., Nigro V., Si
HOX gene family.";
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                                                                                                                                                                                                                                               regulation;
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MISSING (IN ISOFORM 2).

MISSING (IN ISOFORM 2).

DSL -> MCQ (IN ISOFORM 2).

MSCSES -> MFCTRNVSQKGLSAPFAKLSHNNVMLGE

(IN REF. 3).

G -> R (IN REF. 1).

QA -> HR (IN REF. 1).

L -> S (IN REF. 4).

L -> F (IN REF. 4).

R -> P (IN REF. 4).

MW; 20F89542582D6F25 CRC64;
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POLY-PRO.
POLY-PRO.
POLY-GLY.
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Best Local :
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15-JUL-1998
15-JUL-1998
15-DEC-1998
                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                    overlapping
                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                          Modolell J., Gruss P.; "Identification of the vertebrate Iroquois homeobox gene family with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                             EMBL; Y15001; CAA75233.1;
                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
                                                                                                                                                                                                                                                               system.
                                                                                                                                                                                                                                                                                                                        MEDLINE-98145944; PubMed-9486539;
Bosse A., Zulch A., Becker M.B., Torres M.,
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.
              InterPro;
                               MGD; MGI:1197522;
                                                 HSSP; P02833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRX3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPPAPQLNASTSS---TVTGSGGY-----FDLPPSVDSSSSIYALRPIPSPAGATAPADL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGSGGGGGGGGSSEDKMMVSAAAGEGEEVDELLAALGYKVRASDMADVAQKLEQLEMAMG 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGGGGGLGP----GAH-----GYGPSPIDLWLDAPRSCRMEPPDGPPPPPQQQPPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGGGGGGYYAHGGYYLPPAAD------LPYGLQSCGLFPTLGGKRNEAASPG
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IPR001356; Homeobox.
IPR003893; Iroquois_homeo
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(Rel. 36, Last seq
(Rel. 37, Last ann
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7: Irx3.
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Pred. No. 0.46;
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                                                                                                        http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                        Gomez-Skarmeta J.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158;
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                                                                                                                        for commercia.
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oriented open reading frame: characterization of their promoter an enhancer regions.";
Virology 179:365-377(1990).

'I FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.

-I- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-I- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAITOR OTHER PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRVKA
                                                                                                                                                                                                                                           MEDLINE=91021039; PubMed=2171211;
Vlcek C., Kozmik Z., Paces V., Schirm S., Schwyzer M.;
"Pseudorabies virus immediate-early gene overlaps with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation updat
IMMEDIATE-EARLY PROTEIN IE180.
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DOMAIN
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Viruses; dsDNA viruses, no RNA stage; He
Alphaherpesvirinae; Varicellovirus.
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SMART; SM00548; IRO; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPQLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRDPKR 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LARRVFRFRPQPDSSLLDAA 301
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DOMAIN 347 354 POLY-SER.
DOMAIN 379 397 POLY-SER.
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                                  RTVAPLVRYSVDGARAREAAWTYAAALFAPANVAAARLAEAAARPGPAEPAPGLPPLWPE
                                                                     RFTESLHYYS----
                                                                                                      E--RLLPCPLRLPAPARAPAALGPACLEEVTAALLALRDAIPGAGPAERRQAADSVALVA
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"Identification of 10 murine homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
                                                         TRANSFAC; T01715; -.
MGD; MGI:96171; Hoxa10.
InterPro; IPR001356; Homeobox.
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01-OCT-1996 (Rel. 34,
20-AUG-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSDOM
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"Detection of homeobox genes in development and evolution.";
"Detoc. Natl. Acad. Sci. U.S.A. 88:10711-10715(1991).
-I- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 346-370 FROM N.A. STRAIN-C57BL/6; TISSUE-Spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 325-384 FROM N.A. MEDLINE-92073356; PubMed-1683707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benson G.V., Nguyen T.-H.E., Maas R.L., "The expression pattern of the murine H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HXAA_MOUSE P31310;
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MEDLINE=95166244; PubMed=7862151;
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                                                                                                                                                      F38809; F38809.
F37290; F37290.
F; P02833; ISAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTIFIES ON THE ANTERIOR-POSTERIOR AXIS. BINDS TO THE DNA SEQUENCE 5' AA[AT]TTTAATAC-3'.
SUBCELLULAR LOCATION: NUCLEAR ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING LIMB BUD WHERE IS RESTRICTED TO THE MESENCHYME ALONG THE PROXIMAL-DISTAL AXIS.
ALSO FOUND IN DEVELOPING GUT AND UROGENITAL TRACT. IN ADULT TISSUE, BOTH FORMS FOUND IN KIDNEY BUT ONLY ISOFORM 1 IS EXPRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: EMBRYONIC EXPRESSION INCREASES FROM DAY TO DAY 12 AND THEN DECLINES TO DAY 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN SKELETAL MUSCLE
                                   PF00046; homeobox;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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DOMAIN 2
                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                 Murphy L., Harris D., Barrell B.G., Rajandream Submitted (OCT-1996) to the EMBL/GenBank/DDBJ ci- SIMILARITY: BELONGS TO THE PUMILIO/MPT5 FAN
                                                                                                                                                                          SEQUENCE FROM N.A.
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38; Conservative
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Pred. No. 0.
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DSL -> MCQ (IN ISOFORM 2);
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01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation updat
20-AUG-2001 (Rel. 40, Last annotation updat
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00025; Pumilio; 8. Hypothetical protein. SEQUENCE 681 AA; 73292 MW;
                                 adjoining parts of the long unique simplex viruses types 1 and 2."; J. Gen. Virol. 72:3057-3075(1991).
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Pfam; PF00806; PUF; 8.
                                                                  McGeoch D.J., Cunningham C., McIntyre G., Dolan A.; "Comparative sequence analysis of the long repeat radjoining parts of the long unique regions in the g
                                                                                                                                                                                                      Herpes simplex virus (type 2 / strain Viruses; dsDNA viruses, no RNA stage;
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   SEQUENCE FROM N.A.
                                                                                                                   SEQUENCE FROM N.A. MEDLINE=92113549; Pubmed=1662697;
                                                                                                                                                                    Alphaherpesvirinae;
NCBI_TaxID=10315;
                                                                                                                                                                                                                                                                                                                                           ICPO_HSV2H
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                                                                                                                                                                                                                                                                                                                                                                                                                              -----LVSSP----DQISCIVNALRPNVVLLTKDLNGNHVIQKCLNKFSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TRALQKI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LMVDAFGNYLCQKL----FEHASEAQRSTFIQIIAPKL-VPISFNMHG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSVASLSLQNSNILSFCKDQHGCRYLQRLLEKKNQSHIDAVFA-----ETHPYLAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMRKVAAYFGEALA-----RRVFRFRPQPDSSLLDAAFADLLHAHFYESCPYLKFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSKNSSASILQMNTTLDDIPILLRRPGLSSYTPGPSTSRRSISSSSNLGGNPGLIANNPS
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                                                                                                                                                                                      Simplexvirus
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Pred. No. 2.1;
74; Mismatches 135;
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ICPO (VMW118
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Best Local
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01-NOV-1997
30-MAY-2000
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                     Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001841; Znf_ring.
pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
proSITE; PS00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D10471; BAA23427.1; -. EMBL; Z86099; CAB06760.1; -. PIR; JQ1501; EDBEXD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databa:
-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-i- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
                                                                                                                          Q00083;
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           NCBI_TaxID=5072;
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                                                                                                                                                                                                                                                                                                        507
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                                                                                                                                                                                                                                                                                                                             TVHYNP-----TDLSSWVESMLSELNAPPPPLPP-----APQLNASTSSTVTGSGGY 136
                                                                                                                                                                                                                                                                                                                                                                              ASDMADV-----AQKLEQLEM--AMGMGGVGA------GAAPDDSFATHLATD
                                                                                                                                                                                                                                                                                                                                                                                                        SGPGGGGLPQSSGRAARPRAAVAPRVRSPPRAAAAPVVSASADAAGPAPPAVPVDAHRAP 453
                                                                                                                                                                                                                            SSSSSSLGGGARSSVVEAA 207
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197 (Rel.
190 (Rel.
2 PRIMARY
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126 152
152
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6 27
8 1986 MW;
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                                                                        35, Created)
35, Last sequence update)
39, Last annotation update)
STERIGMATA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.9%;
25.9%;
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POLY-GLY.
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POLY-SER.
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POLY-SER.
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Pred. No. 2.
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                                                                                                                                       1676 AA
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                                   Eurotiomycetes;
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SEQUENCE
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DOMAIN
 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=98025472; PubMed=9379904; Suelmann R., Sievers N., Fischer R.; Suelmann R., Sievers N., Fischer R.; "Nuclear traffic in fungal hyphae: in vivo stud and positioning in Aspergillus nidulans."; Mol. Microbiol. 25:757-769(1997).

-1- FUNCTION: REQUIRED FOR NUCLEAR POSITIONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Aspergillus nidulans apsA (anucleate primary sterigmata) encodes a coiled-coil protein required for nuclear positioning and completion
                                                                                                                                                                                      1109
                                                                                                                                                                                                                                                  1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95164553; PubMed=7860626; Fischer R., Timberlake W.E.;
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Cell Biol. 128:485-498(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASEXUAL DEVELOPMENT.
SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED
                                                                                                                       TADGLYTQQNGYTLPLGAISGNAAPRRARS
                                                                                                                                                                                                                                                                                ------LPPAPQLNASTSST
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                                                                                                                                                                                                                                                                                                                                                                                                    GSSEDKMMVSAAAGEGEEVDELLAALGYKVRASDMADVAQKLEQLEMAMGMGGVGAGAAP
 AASQASSVQ--
                              AASQGGAMRKVAAYFGEALARRVFRFRPQPDSSLLDAAFADLLHAHFYESCPYLKFAHFT
                                                           RPLSPPDSDKLNEMSNSP
                                                                                        VEAAPPVAAAANATPALPVVVVDTQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPLL
                                                                                                                                                                                    VETPPVQYTPDVLILPTPPALDENTP-----PSVMASTAKATKSAPPLVVVDDNTDKG 1161
                                                                                                                                                                                                                                                EPIREAKEEAAAVDDVASESTHPVLSIFLTPPAYTEPTAPKLQEAVIPPAPQLALSTVSS
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N 51 127
N 193 359
N 408 453
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1676 AA;
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AA; 183671 MW;
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Pred. No. 7.
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
PH.
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                                                                                                                         -GSSNQADQGAQTILSSKQIDQLLIDRASV 1220
                                                             -FATPKARSRPVPQASNASLHKRPGS
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AND
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075962; Q13458;
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20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 1227-1407, AND MUTAGENESIS.
MEDITRE-99005194; PubMed=9790533;
Liu X., Wanng H., Eberstadt M., Schnuchel A., Olejniczak E.T.,
Meadows R.P., Schkeryantz J.M., Janowick D.A., Harlan J.E.,
Harris E.A.S., Staunton D.E., Pesik S.W.;
"NMR structure and mutagenesis of the N-terminal Dbl homology domain
of the nucleotide exchange factor Trio.";
Cell 95:269-277(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                              expression promotes actin cytoskeleton reorganization, and anchorage independent cell growth.";
J. Cell Sci. 112:1825-1834(1999).
                                                                                                                                                 Seipel K., Medley Q.G., Kedersha N.L., Zhang X.A. Serra-Pages C., Hemler M.E., Streuli M.; "Trio amino-terminal guanine nucleotide exchange
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRIPLE FUNCTIONAL
                                                                                                                                                                                                      MEDLINE=99276567;
                                                                                                                                                                                                                      CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                   FOR CELL SUBUNIT:
                               FUNCTION: PROMOTES THE EXCHANGE OF GDP BY LEUCOCYTE ANTIGEN-RELATED (LAR) PROTEIN, I COORDINATING CELL-MATRIX AND CYTOSKELETAL FOR CELL MIGRATION AND CELL GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRMIQAITQ-----TMIGEFLWKYTRRAVSGEI-----SNTRHRRYFWVHPYTRTL--YW 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQVGSAKTTTSRASVRRDSHMSRRSSVSSFASELEERFNMQP----NPPFAPQGYSTGTD 1384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ase, contains a protein kinase domain, and has separand rho-specific guanine nucleotide exchange factor
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                                                                                                                                                                                                      PubMed=10341202;
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Last annotation updat
                   FORM A COMPLEX WITH LEUKOCYTE ANTIGEN RELATED
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                                                                                                                                                                                   Zhang X.A., O'Brien S.P.,
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                                                  REARRANGEMENTS
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                                                  NECESSARY
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   Pfam; PF00621; RhoGEF; 2.
Pfam; PF000435; SPectrin; 7.
Pfam; PF000435; Spectrin; 7.
SMART; SM00408; IGC2; 1.
SMART; SM00233; PH; 2.
SMART; SM00235; RhoGEF; 2.
SMART; SM00325; RhOGEF; 2.
SMART; SM00316; SEC14; 1.
SMART; SM00316; SEC14; 1.
SMART; SM00320; STRC; 6.
SMART; SM00220; STRC; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_C2.
InterPro; IPR001849; PH.
InterPro; IPR001919; RhoGEF.
InterPro; IPR001452; SH3.
InterPro; IPR002290; Ser_thr_kin_ac_InterPro; IPR002017; Spectrin.
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Transferase; Serine/threonine-protein kinase; ATP-binding,
Immunoglobulin domain; SH3 domain; Alternative splicing.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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DOMAIN
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                                                                                                                                     REPEAT
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
ified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE RHO/RAC GEF FAMILY.

SIMILARITY: CONTAINS 2 DBL-HOWOLOGY DOMAINS (DH).

SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 PH DOMAINS.

SIMILARITY: CONTAINS 1 SH3 DOWAIN.

SIMILARITY: CONTAINS 1 SPECTRIN REPERATS.

SIMILARITY: CONTAINS 4 SPECTRIN SECTION; BELONGS TO THE SER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE, BRAIN, PANCREAS, PLACENTA, LIVER, KIDNEY AND LUNG.
BRAIN, PANCREAS, PLACENTA, LIVER, KIDNEY AND LUNG.
DOMAIN: THE N-TERMINAL DBL/GEF DOWAIN SPECIFICALLY CATALYZES NUCLEOTIDE EXCHANGE FOR RAC1, LEADING TO THE ACTIVATION OF JUNKINASE AND THE PRODUCTION OF MEMBRANE RUFFLES. THE SECOND DBL/G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN IS AN EXCHANGE FACTOR STRESS FIBERS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00069; pF00621;
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PS00107; PROTEIN_KINASE_ATP; FAI
PS00108; PROTEIN_KINASE_ST; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
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   SH3; 1.
   spectrin; 7.
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Spectrin.
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IG-LIKE C2-TYPE DOMAIN.
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Ol-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN
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                          (Chinese hamster)
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POPVRHHPPVLVSSAASSQABADKMS -> AAAGVGAAAAA
GPPVAAAATVAAPAAAAAPPARAGAGPPGSPSLSDTTPPCW
SPLQPBARQRCTRCQ (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVITY.
T->A: 80% DECREASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 123.5;
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E->A: 30% DECREASE IN NUCLEOTIDE EXCHANGE
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Best Local Similarity 19.9
Matches 119; Conservative
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1307:21-25(1996).

Biochim. Biophys. Acta 1307:21-25(1996).

CHROMOSOMES AND BINDS TO A SPECIFIC SUBSET OF ALPHOID SATELLITE DNA, CALLED THE CENP-8 BOX. MAY ORGANIZE ARRAYS OF CENTROMERE SATELLITE DNA INTO A HIGHER ORDER STRUCTURE WHICH THEN DIRECTS CENTROMERE FORMATION AND KINETOCHORE ASSEMBLY IN MANMALIAN CHROMOSOMES (BY SIMILARITY).

-!- SUBGELLULAR LOCATION: NUCLEAR.
-!- SUBGELLULAR LOCATION; WITH OTHER MAMMALIAN CENP-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning of an intronless antigen CENP-B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96254058; PubMed=8652663; Bejarano L.A., Valdivia M.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                  DPNEEPEVIAVNSVFEMHRLLAQPGALEKVLGTVRAVRPRIVTVVEQEANHNSGTFLDRF
                                                                                                                                RLTGVGPPQPDETDALQQV--GWKLAQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGEE
                                                                                                                                                                                                                                                              TQALAKYLKALDTRMAAESRRVLLLAGRLAAQSL-----DTS-----GLRHVQL--
                                                                                                                                                                                                                                                                                                  AEALVKQIPLLAASQGGAMRKVAAYFGEALARRVFRFRPQPDSSLLDAAFADLLHAHFYE
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                              EEEEEEE-
                                                                                                                                                                                                                                                                                                                                          LSVLLCANRDGSEKLPPLVAGKSAKP-------RASQGGLPCDYTANSKGGVT
                                                                                                      LQLGL-----VEALHEVAAAWQAVEPA-DIATCFREAGFGGGLNATITT-SFKSEGEE
                                                                                                                                                                                                                      SCPYLKFAHFTANQAILEAFAGCRRVHVVDFGIKQGM----QWPALLQALALRPGGPPSF
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Q61548; Q61547;
Q61548; 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 40, Last annotation update)
CLATHRIN COAT ASSEMBLY PROTEIN AP180 (CLATHRIN COAT ASSOCIATED PROTEIN AP180) (PHOSPHOPROTEIN F1-20) (91 KDA SYNAPTOSOMAL-ASSOCIATED
AP180) (PHOSPHOPROTEIN F1-20) (91 KDA SYNAPTOSOMAL-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINK CLATHRIN TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN COMPLEXES ARE COMPONENTS OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION. BINDING OF AP180 TO CLATHRIN TRISKELIA INDUCES THEIR ASSEMBLY INTO 60-70 NM COATS.

1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE CYTOPLASMIC FACE OF COATED VESICLES IN THE PLASMA MEMBRANE.

1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

1- TISSUE SPECIFICITY: BRAIN. ASSOCIATED WITH THE SYMAPSES.

1- DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED IN A PATTERN COINCIDENT WITH ACTIVE SYNAPTOGENESIS AND SYNAPTIC MATURATION.

1- DOMAIN: POSSESSES A THREE DOMAIN STRUCTURE: THE N-TERMINAL 300 RESIDUES HARBOR A CLATHRIN BINDING SITE, AN ACIDIC MIDDLE DOMAIN 450 RESIDUES, INTERROUTED BY AN ALA-RICH SEGMENT, AND THE C-TERMINAL DOMAIN (166 RESIDUES).
                                                                                          DOMAIN
DOMAIN
DOMAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Neurosci. 12:2144-2155(1992).
                                                                                                                                                                                                                                                            MGD; MGI:109132; Snap91.
InterPro; IPR001026; ENTH.
Pfam; PF01417; ENTH; 1.
SMART; SM00273; ENTH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M83985; AAA37587.1; -. EMBL; M83985; AAA37586.1; -.
                                                                                                                                                                                                                             Coated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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POLY-THR.
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   W.
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POLY-SER.
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MISSING (IN SHORT ISOFORM).
   24A98FBACE8DB8B1 CRC64;
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                                                                                                                                                                                                                                                                                                         Ustilago maydis (Smut fungus).
Eukaryota; Fungi; Basidiomycot
Ustilaginomycetidae; Ustilagin
CBI_TaxID=5270;
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                                                                                                                                                        3old S., Duncan G., Barrett K., Kronstad J.W.;
¹cAMP regulates morphogenesis in the fungal pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 PCEAPISDPFAPEPSPPTTTTEPA-SASASTTTAVTA-----VTTEVDLFGDAFAASPG 445
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     CATALYTIC ACTIVITY: ATP - 3',5'-CYCLIC AMP
                                                                                   FUNCTION:
                                                        METABOLISM
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                                                        ВУ
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40,
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                                                        CATALYSING
                                                                                                                                                                                                           PubMed=7995519;
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22.7%;
                                                                                ESSENTIAL
                                                                                                                                                                                                                                                                                                                                         Ustilaginales; Ustilaginaceae;
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Last annotation update)
4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
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SMART; SM00369; LRR_TYP;
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                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
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                                                                                                                                                                                                                                              REPEAT
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                   100
                                  170 SDGDVGKAVQSANHQDISPFLFQSE-----NAAPFSS-----SHSNRTSVN 210
211 PSAASTASPSTSAATRTRPRGGTNASQYNTLDTSFGSID-RPGLSSSRSQYSLRPQTPPS 269
                                                                                                            Local Similarity
wes 66; Conserv
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- SIMILARITY:
- SIMILARITY:
          SWVESMLSELNAPPPPPLPPAPQLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPA 159
                                                                       QDRSSSGSGSGSGSRSYFPANSHSDSLPGPSTHSISPSFDE-DELRQIMSHIPANQATSS 169
                                                                                           QDAGGSGGGGG------MGSSEDKM-----MVSAAAGEGEEVDELLAAL-----
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                                                     -GYKVRASDMADVAQKLEQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLS
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1633
                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            LRR_TYP; 2.
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PP2C_catalytic.
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POLY-ASP.
                                                                                                                                                                                                                                                     Score 119.5;
Pred. No. 21;
                                                                                                                                                                   PP2C-LIKE.
CATALYTIC.
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LRR 16.
LRR 17.
LRR 18.
LRR 19.
LRR 20.
LRR 21.
                                                                                                             Mismatches
                                                                                                                                                           106A872C3C1C5BF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       cAMP synthesis; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                DB 1;
                                                                                                             106;
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                                                                                                             Indels 71;
                                                                                                                                Length 2493;
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Gapop 10.0 , Gapext 0.5
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1 MKREYQDAGGSGGGGGGGGGS.....TLGWHTRPLIATSAWRLAGP 623
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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599	600.5	604.5	606	670	1005.5	1450.5	1495.5	1511.5	1530.5	1590	1594	1594	1604	1608	1612	2669	2683	3194	Score
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	Q96304 arabidopsis	Q9m384 arabidopsis	Q91wu9 oryza sativ	Q9fuz7 zea mays (m	Q9as97 oryza sativ	Q9lf53 arabidopsis			Q9srp9 arabidopsis	O23643 arabidopsis	Q9lqt8 arabidopsis	O23724 arabidopsis	O23725 arabidopsis	Q9slh3 arabidopsis	O23642 arabidopsis	Q9mb96 oryza sativ	Q9st48 zea mays (m	Q9st59 triticum ae	Description

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Q9suf	O9m0m5	08093	Q9xe5	023566	Q9xe5	Q9szf	Q91ti5	Q9xe58	Q9scr0	081074	Q91nx6	Q9xe51	0950	Q9xe5	Q9ztb1	Q9fhz1	Q9arf6	Q9f103	Q9zwc	Q9can3	Q9s7	Q91pt0	Q91 <sub>E</sub>	Q9avk4	/ TDT 67
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## ALIGNMENTS

	Db 121 QLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRDPKRMRT 180
	Qy . 121 QLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRDPKRMRT 180
	Db 61 EQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPPPLPPAP 120
	Qy 61 EQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPPPLPPAP 120
	Db 1 MKREYQDAGGSGGGGGMGSSEDKMMYSAAAGEGEEVDELLAALGYKVRASDMADVAQKL 60
	Qy 1 MKREYQDAGGSGGGGGGGGGSSEDKMMVSAAAGEGEEVDELLAALGYKVRASDMADVAQKL 60
0;	Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps
	Match 100.0%;
	RL Nature 400:256-261(1999). DR EMBL: AJ242531: CAB51555.1:
	modulators.";
	"'Green revolution' genes encode mutant gibberellin respo
	Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd
	RA Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F.,
	MEDLINE=99347734; PubMed=10421366;
	OX NCBI_TaxID=4565;
	Triticeae; Triticum.
	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	DE GIBBERELLIN RESPONSE MODULATOR.
	01-MAY-2000 (TrEMBLrel. 13, Last
	AC Q9ST59; FRELIMINARI; FRI; 025 AA.
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MEDLINE-99347734; PubMed-10421366;

Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,

Peng J., Richards D.E., Fish L.J., Worland A.J., Pelica F.,

Flintham J.E., Beales J., Fish L.J., Worland A.J., Harberd N.P.;

Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;

Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;
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NON_TER
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                                                                                                                                                                                                                                                                       Nature 400:256-261(1999).
EMBL; AJ242530; CAB51557.1;
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RESPONSE MODULATOR (FRAGMENT).
                                                                                                                                                                    Conservative
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7; Mismatches 37;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.

NCBI_TaxID-4530;
                                                                              Gene 245:21-29(2000).
EMBL; AB030956; BAA90749.1; -.
SEQUENCE 625 AA; 65406 MW;
                                                                                                                 STRAIN-CV. NIPPONBARE;

MEDLINE-20179680; PubMed-10713441;

Ogawa M., Kusano T., Katsumi M., Sano H.;

"Rice gibberellin-insensitive gene homolog, (
localized protein capable of gene activation
                                                                                                                                                                                                                             OSGAI.
                                                                                                                                                                                                                                      OSGAI
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                                   Conservative
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                                                                                                                                                                                                                                             Created)
Last sequence up
Last annotation
                                   Score 2669; DB 10;
Pred. No. 7.9e-165;
4; Mismatches .47;
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                                                                    Query Match
Best Local Similarity
Matches 340; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O23642 PRELIMINARY;
O23642;
O1-JAN-1998 (TrEMBLrel. 05,
O1-JAN-1998 (TrEMBLrel. 05,
O1-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=97379310; PubMed=9237632;

Truong H.N., Caboche M., Daniel-Vedele F.;

Truong H.N., Caboche M., Daniel-Vedele F.;

"Sequence and characterization of two Arabidopsis isolated by functional complementation of a yeast |

FEBS Lett. 410:213-218(1997).

EMBL; Y11336; CAA72177.1; -.

Mendel; 24145; Arath; 3051;24145.

Mendel; 24145; Arath; 3051;24145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Ewkaryota; Viriddiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MKREYQDAGG----SGGGGGGMGSSEDKMMV--SAAAGEGEEVDELLAALGYKVRASDMA
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Pred. No. 1.8e
2; Mismatches
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STRAIN-CV. COLUMBIA;

MEDLING-2008487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.

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Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome II of Arabidopsis thaliana.";

Nature 402:761-768(1999).

EMBL; AC005560; AAC673331; -.

ESEQUENCE 587 AA; 64035 MW; FC92E7F9408072AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               AT2GO1570.

AT2GO1570.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eucosids II; Brassicales; Brassicaceae; Arabidopsis.
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Q9SLH3;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Last annotation updat
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                                                                                                                                                              Somerville C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosidae;
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Best Local S
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023725;
01-JAN-1998
01-JAN-1998
01-NOV-1999
                                                                                                 GRS PROTEIN.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
 Murphy G.P., Harberd N.P.;

Genes Dev. 0:0-0(0).

EMBL; X15194; CAA75493.1; -.

Mendel; 24071; Arath;3051;24071.

Mendel; 24071; Arath;3051;24071.
                                                        Peng
                                                                    STRAIN-COLUMBIA;
                                                                              SEQUENCE FROM N.A.
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                                                        Carol P.,
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                                              Richards
erd N.P.;
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Last sequence up
Last annotation
                                                        D.E.,
   F6F6C7738EE7DCA9
                                                       King
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                                                         X.E.,
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                                                         Cowling
   CRC64;
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                                                         R.J
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Best Local S
Matches 338
SEQUENCE FROM N.A.

STRAIN-LANDSBERG ERECTA;

STRAIN-LANDSBERG ERECTA;

MEDLINE-98051192; PubMed-9389651;

Peng J., Carol P., Richards D.E., Ki
Murphy G.P., Harberd N.P.;

"The Arabidopsis GAI gene defines a
regulates gibberellin responses.";

Genes Dev. 11:3194-3205(1997).
                                                                                                                                                                                               023724;
023724;
01-JAN-1998
01-JAN-1998
01-MAY-2000
                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                             NCBI_TaxID=3702;
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                                                                                                                                                                                      PROTEIN
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                                                                                                                                                                                                                                                                                                                     AGGDGYKVEEKEGCLTLGWHTRPLIATSAWRLA 621
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Q9LQT8;
Q1-OCT-2000
01-OCT-2000
01-OCT-2000
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Wall
Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Wall
Hilliams S., Altafi H., Araujo R., Conn L., Conway A.B., Gon:
Williams S., Huizar L., Kremenetskaia I., Lenz C., Li J., Li
Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Li
Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V.,
                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidi
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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Mendel; 24070; Arath;3051
SEQUENCE 532 AA; 58789
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AA; 58789 MW;
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Pred. No. 2.4e-95;
1; Mismatches 106;
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EMBL; AC006917; AAF79228.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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Pred. No. 2.4e-95;
1; Mismatches 106;
                                                                                       ----VPSGQDKVMSEVYLGKQICNVVACDGPDRV
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O23643;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JAN-1999 (TrEMBLrel. 12, Last annotation update)
RGA2 PROTEIN.
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EMBL; Y1133; CAA72178.1; ....

Mendel: 24146; Arath;3051,24146.

SEQUENCE 532 AA; 58789 MW; 17AC719CA8072239 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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hes 331;
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                                                                                                                                                                                HYYSTLFDSLEG----
                                                                                                                                                                                                                                                                                             EIESVAVNSVFELHKLLGRPGAIDKVLGVVNQIKPEIFTVVEQESNHNSPIFLDRFTESL
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Pred. No. 4.3e-95;
2; Mismatches 100
                                                                                                                                                                            - VPSGQDKVMSEVYLGKQICNVVACDGPDRV
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Query Match
Best Local Similarity
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"Arabidopsis thaliana chromosome III BAC T21P5 genomic sequence.";
Submitted (OCT-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AC009895; AAF01590.1;
SEQUENCE 547 AA; 60493 MW; C4D18D5951D95634 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyla;eone eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAY-2000 (TrEMBLrel. 13, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. COLUMBIA;
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VAATLADLEPFMLQPEGEEDPNEEPEVIAVNSVFEMHRLLAQPGALEKVLGTVRAVRPRI
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                                                                                           VTVVEQEANHNGIVFLDRFNEALHYYSSLFDSLE--DSYSLPSQ---
                                                                                                                      VTVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEGGSSGGGFSEVSSGAAAAPAAAGTDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.9%; Score 1530.5; DB 51.3%; Pred. No. 3.2e-91;
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway J.-D., Fong B., Fujii C.Y.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Liee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Mu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
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01-JUN-2001
01-JUN-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:816-820(2000).
EMBL; AC020665; AAG52171.1;
SEQUENCE 511 AA; 56754 M
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                                                                                                                                                                                                                                                                                                                  EQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPPPPLPPAP 120
AFADLLHAHFYESCPYLKFAHFTANQAILEAFAGCRRVHVVDFGIKQGMQWPALLQALAL
                                                           QLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRDPKRMRT 180
                                                                                                                                                                                                                                                                                                                                                                             MKREHNHRESSAGEGG--SSSMTTVIKEEAAG----VDELLVVLGYKVRSSDMADVAHKL
                                                                                                                                                                                                                                                                                                                                                                                                                  MKREYQDAGGSGGGGGGGGSSEDKMMVSAAAGEGEEVDELLAALGYKVRASDMADVAQKL 60
                                                                                                  CAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALARRVFRFRPQPDSSLLDA
                                                                                                                                        ESELSSTRS-------VVVLDSQETGVRLVHALLA
                                                                                                                                                                                                                                                                                                EQLEMVLGDG -----ISNLSDETVHYNPSDLSGWVESMLSDLD -- PTRIQEKP
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.38;
52.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52171.1; -. 56754 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1511.5; DB Pred. No. 4.9e-90;
                                                                                                                                                                                                                      -DSEYDLRAI -- PGSAVYPRD -- EHVTRRSKRTRI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 118; Indels 113; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1E60071697C92A9F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 511;
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                                                                                                  300
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RESULT

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Best Local s
Matches 320
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01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning of the Arabidopsis thaliana RGA-like gene, a putative member of the VHIID domain transcription factor family,"; submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ224957; CAAL2242.1; -

Mendel; 29006; Arath; 3051; 29006.

InterPro; IPR001680; WD40.

Pfam; PF00400; WD40; 1.

SMART; SM00330; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=CV. COL-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  065367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanchez-Fernandez R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50082; WD_REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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  182
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                                                                                                                                                                                     QLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPPPLPPAPQ
GSSTSSSSSSSSSIGGGARSSVYEAAPPVAAAANATPALPVVVVDTQEAGIRLVHALLAC
                                                                                                        LNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRDPKRMRTG
                                                                                                                                                            QLEMVLGDG------ISNLSDETVHYNPSDLSGWVESMLSDLD--PTRIQEKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFLDRFTESLHYYSSLFDSLE-----GPPSQ-----
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                                                                                                                                                                                                                                                                                                                                                                       al Similarity 51.7
320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 AA; 73126 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                46.8%;
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                                                    ----DSEYDLRAI--PGSAVYPRD-----EHVTRRSK
                                                                                                                                                                                                                                                                                                                                                                          68;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    Score 1495.5;
Pred. No. 7.4e-
68; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 662;
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Best Local Similarity
Matches 313; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/G
EMBL; AL391150; CECO1893.1; -.
SEQUENCE 523 AA; 57326 MW; 0F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.Y., Kaneko T., Kato T., Asamizu E., Ko Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Ko Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                                        CLTLGWHTRPLIATSAWRL
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                         SELNAPPPPLPPAPQLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPAD
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                         Score 1450.5; DB 10;
Pred. No. 4.5e-86;
6; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        OF6CEOBD13403C35 CRC64;
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RESULT
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Best Local S
Matches 222
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Q9AS97;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome
"Cone:P0707D10.";
"Clone:P0707D10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice). Oryza sativa (Rice) Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP002910; BAB40172.1; - SEQUENCE 493 AA; 51864 MW; 5FDB670EB8899492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUTATIVE OSGAI.
P0707D10.30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                           Local Sir
hes 222;
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                                                                                                                                                                                         PPPLPPAPQLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSV
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                                                                             RDPKRMRTGGSSTSSSSSSSSSLGGGARSSVVEAAPPVAAAANATPALPVVVVDTQEAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYTYVEQEANHNGDVFLDRFNEALHYYSSLFDSLEDG----
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                                                                                                                                                                                                                                           Similarity 43.1
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIPPONBARE;
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(TremBLrel. 17, Last seg
(TremBLrel. 17, Last ann
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                                                                                                                                                                                                                                           31.5%; Score 1005.5; DB
43.1%; Pred. No. 2.6e-57;
tive 64; Mismatches 136
                                                                                                                                            ---DGVGXYDPPAGADVDAA-----ALPEFAAAFPP------
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Last annotation updat
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                                                  -CAPDAAAA - - - - - VLAMRREEEEVAGI
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RESULT 15
Q9FUZ7
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AC Q9FUZ7
AC Q9FUZ7
DT 01-MAR
DT 01-MAR
DT 01-MAR
DT 01-MAR
OC SCR.
OS Zea ma
OC Eukary
OC Sperma
OC Panico
OX NCBILT
RN [1]
RP SEQUEN
RX MEDLIN
RX MEDLIN
RX MEDLIN
RA Lim J.
RA Lim J.
RA Dien
RT "MOlec
RT "MOlec
RT EMBL;
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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Q9FUZ7;
01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                         "Molecular analysis of the SCARECROW gene in maize reveals a common basis for radial patterning in diverse meristems."; Plant Cell 12:1307-1318(2000).

EMBL; AF263457; AAG13663.1; -.
SEQUENCE 668 AA; 71162 MW; 92B7431046B2B621 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=20407145; PubMed=10948251;
Lim J. Helariutta Y., Specht C.D., Jung J., Sims L.,
Diehn S., Benfey P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCARECROW.
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PPLPDKRRHEHPPPCQQQQQEEPHPAPQSPKAPTAEETAAAAAAAAQAAAAAAAKERKEEQ 287
                                  DSVRDPKRMRTGGSSTSSSSSSSSSSSIGGGARSSVVEAAPPVAAAANATPALPVVV---- 224
                                                                         AADPAPLPPPPQ-
                                                                                             NAPPPPLPPAPQLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSA 169
                                                                                                                                                                                SDMADVAQKLEQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESML-SEL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMAEAYLQREICDIVCGEGAARRERHEPLSRWRDRLTRAGLSAVPLGSNALRQARMLVGL 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEGGSSGGGPSEVSSGAAAAPAAAGTDQ 527
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                                                                                                                                                                                                                       AAAAGVGGSGAPSSASAQLPALPTQLHQLPPAFQHHAPEVDVPAHPAPAAHAQAGGEATA 138
                                                                                                                                                                                                                                                        AGGSGGGGGGGMGSSEDKMMVS------AAAGEGEEVD-----ELLAALGYKVRA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLDEVRPWMLQ-----IAPGEAVAFNSVLQLHRLLGDPADQAPIDAVLDCVASVRPKI 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STTAWVDGIIRDI---IGSSG---GAAVSITQLIHNVREIIHPCNPGLASLLELRLRSLL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 16, Created)
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                                                                     ----PQQHALLHGAPAAAPAGLTLP---PP
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GFRAASLAGSAAAQASLLLGMFP-SDGYTLVEENGALKLGWKDLCLLTASAWR
                                                                                                                                                                                                                                                     LAQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGEEDPNE----EPEVIAVNSVFEMHRL
                                                                                          GGPSEVSSGAAAAPAAAGTDQVMSEVYLGRQICNVVACEGAERTERHETLGQWRNRLGNA
                                                                                                                                            YDVTGSDSNTLWLIQRLAPKVVTMVEQDLSH-SGSFLAREVEAIHYYSALFDSLDASYGE
                                                                                                                                                                                                                                                                                                          AFAGCRRVHVVDFGIKQGMQWFALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWK
                                                                                                                                                                                                                                                                                                                                                            SARLVSSCLGLYAPLPPGS----PAAARLHGRVAAAFQVFNGISPFVKFSHFTANQAIQE
                                   GFETVHLGSNAYKQASTLLALFAGGDGYKVEEKEGCLTLGWHTRPLIATSAWR 619
                                                                      DSPER-----GDVKFGSWREKLAQS
                                                                                                                                                              LAQPGALEKVLGTVRAVRPRIVTVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEGGSSG
|: | :: |::||:||: | ||:|| || |::||||:||||:||||
                                                                                                                                                                                                                                                                                      AFEREERVHIIDLDIMQGLQWPGLFHILASRPGGPPRVRLTGLGA----SMEALEATGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VDTQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEAL
                                                                                                                                                                                                                    LSDFADTLGLPFEFCAVA------EKAGNVDPEKLGVTRREAVAVHWLH--HSL
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Search completed: Job time: 337 sec January 22, 2002, 16:30:02

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Result
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Maximum Match 100%
Listing first 45 summaries
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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Best Local
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LENGTH: 282
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CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: PC7GB97/00390
EARLIER FILING DATE: 1997-02-12
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APPLICANT: Peng, Jinrong
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI
FILE REFERENCE: 620-45
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana 09-117-853-8
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SOFTWARE: PatentIn Ver. 2.0
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284 RRVFRFRPQPDSSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEAFAGCRRVHVVDF
                                                               224 VVDTQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALA 283
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                                              LVDSQENGVRLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALA
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LENGTH: 259
TYPE: PRT
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Best Local Similarity
Matches 135; Conserv
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 CURRENT APPLICATION NUMBER: US/09/117,853
CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: PCT/GB97/00390
EARLIER FILING DATE: 1997-02-12
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nilarity 45.2%;
Conservative 3
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GENERAL INFORMATION:
APPLICANT: Harberd, Nicholas P
APPLICANT: Peng, Jinrong
APPLICANT: Carol, Pierre
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI gene
FILE REFERENCE: 620-45
                                                                                                                                                                                                 Sequence 4, Application US/09117853 Patent No. 6307126
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APPLICANT: Beng, Jinrong
APPLICANT: Peng, Jinrong
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI gene of Arabidopsis thaliana
FILE REFERENCE: 620-45
CURRENT APPLICATION NUMBER: US/09/117,853
CURRENT FILING DATE: 1996-08-12
EARLIER APPLICATION NUMBER: PCT/GB97/00390
EARLIER FILING DATE: 1997-02-12
EARLIER FILING DATE: 1998-08-12
EARLIER FILING DATE: 1996-02-12
NUMBER OF SEQ ID NOS: 12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 8.6e-40;
Nismatches 52;
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; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-117-853-4
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EARLIER FILING DATE: 1997-02-12
EARLIER APPLICATION NUMBER: GB 9602796.6
EARLIER FILING DATE: 1996-02-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 166
                                                                                                                                                         Query Match 4.9%; Score 155.5; DB 4; Best Local Similarity 25.7%; Pred. No. 1.5e-05; Matches 61; Conservative 27; Mismatches 50;
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CURRENT FILING DATE: 1998-08-12
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EARLIER FILING DATE: 1996-02-12
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 PLPPAPQLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRD 174
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                                                                          DVAQKLEQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPP 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------GDAIL- 93
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                                      PLPPAPQLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NQFAIDSASSSNQGGGGDTYTTNKRLKCSNGVVE----TTTATAESTRHVV 140
-SSNAEYDLKAIP---
                                                                                                                                                                                                  DB_4; Length 166;
                                                                                                                                                             Indels 99;
----GDAIL- 93
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US-08-804-227C-12
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.0%; Score 127.5; DB 2; Best Local Similarity 21.8%; Pred. No. 0.12; Matches 154; Conservative 72; Mismatches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION UNMBER: US/08/804.22
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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LENGTH: 1891 amino aci
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                                            514 EGTGGGS-GLVVPAADIGYSLATTRETLEHRAVALVQENRTAGEDLAALAAGRTPESVVT 572
                                                                                                                                                                              136 YFDLPPSVDSSSSIYALRPIPS-PAGATAPAD--LSADSVRDPKRMRTGGSSTSSSSSSS 192
                                                                                                                                                                                                                                                                                                                347 ALGDPIEAGALLATYG-RERVGDPLWLGSLKSNIGHAQAAAGVGGVIKVVQAMRHGSLP- 404
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                                                                                                                                                                                                                                                                                                                                          30 AAGEGEEVDELLAALGYKVRASD---MADVAQKLEQLEMAMGMGGV------GAGAAPD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                     80 DSFATHLATDTVHYN-PTDLSSWVE---SMLSELNAPPPPLPPAPQLNASTSSTVTGSGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCI(DOS) Text only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
VVDTQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAAYFGEALA 283
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No. 5876991
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                                                                                         SSLGGGARSSVVEAA-----
                                                                                                                                    HVVLEEAPVEAGSEHGDGPGPDRPDAVTGPLPWVLSARS-REALRGQAGRLAALARQGRT 513
                                                                                                                                                                                                                           -----RTLHVDAPSSKVEWASGAVELLTEGRSWPRRVERVRRA-AVSAFGVSGTNA 454
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                                                                                         -PPVAAAANATPALPVV 223
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US-08-804-198-6
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                                                                                         TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Macintosh; SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Richardson, Mark A.
APPLICANT: ROSteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          933 APASAAVAPATAAPSVRSVPEAEQDGALWAAVHAGD-VASAAARL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        874 VVFAPALRRGRPEGDTVLRAAASAYVRGAGL-DWAALYGGTGARRTDLPTYAFQHSRYWL
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                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/804,198 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: LILLY CORPORTY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                             REGISTRATION NUMBER: 36,470 REFERENCE/DOCKET NUMBER: P9:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                       TOPOLOGY:
                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                         LENGTH:
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LILLY CORPORATE CENTER
                                                                         1891 amino acids
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                                       unknown
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Sequence 11, Application US/08804227C

Patent No. 5876991

GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Sutton, Kinberly L.
APPLICANT: Sutton, Kinberly L.
APPLICANT: Sutton, Kinberly L.
CORRESPONDENCE ADDRESS: 15
CORRESPONDENCE ADDRESS: 15
CORRESPONDENCE ADDRESS: 15
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER

STATE: COUNTRY:

RY: USA 46285

INDIANAPOLIS IN RESULT 8 US-08-804-227C-11

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Best Local Similarity 21.8%; Pred. No. 0.12;
Matches 154; Conservative 72; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193
933 APASAAVAPATAAPSVRSVPEAEQDGALWAAVHAGD-VASAAARL
                                                                            874 VVFAPALRRGRPEGDTVLRAAASAYVRGAGL-DWAALYGGTGARRTDLPTYAFQHSRYWL
                                                                                                                                                          814 LADAAQLTDPGYWTRQVRQPVRFADAVRTASARDAATFIELGPDAVLCGMAEESLAAEAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573 GVARRGRGI----AFLCSGQGAQR--LGAGRELRGRFPVFA----DALDEIAAEFDAHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 DSFATHLATDTVHYN-PTDLSSWVE---SMLSELNAPPPPLPPAPQLNASTSSTVTGSGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 AAGEGEEVDELLAALGYKVRASD---MADVAQKLEQLEMAMGMGGV-----GAGAAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVVLEEAPVEAGSEHGDGPGPDRPDAVTGPLPWVLSARS-REALRGQAGRLAALARQGRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGTGGGS-GLVVPAADIGYSLATTRETLEHRAVALVQENRTAGEDLAALAAGRTPESVVT
                                    --ASTLLALFAGGDGYK----VEEKEGCLTLGWHTRPLIATSAWRL
                                                                                                                    QVMS-EVYLGRQICNVVACEGAERTERHETLGQWRNRLGNAGFETVHLGSNAYKQ-----
                                                                                                                                                                                                                                           -----LRVSHAFHSPRMDAMLADFRAVADTVDYHAPRLPVVSEV-----TGD
                                                                                                                                                                                                                                                                               PEGEEDPNEEPEVIAVNSVFEMHRLLAQPGALEKVLGTVRAVRPRIVTVVEQEANHNSGT
                                                                                                                                                                                                                                                                                                                                                               -GGPPSFRLTGVGPPQPDETDALQQVGWKLAQFAHTIRVDFQYRGLVAATLADLEPFMLQ
                                                                                                                                                                                                                                                                                                                                                                                                          LVAAHVAGVFSAADAARLVSARGRLMRALPEGGAMAAVQATEREAAALEPVAAGGAVVAA 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKFAH----FTANQAILEAFAGCRRVHVVDFGIKQGMQWPALLQALALRP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPLLSVMFAEPATPDAALLDRTDYTQPALFAVETALFRLLESWGLVPDVLVGH---SIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RR----VFRFRPQPDSSLLD------AAFA--------DLLHAHFYESCPY 316
                                                                                                                                                                                                  FLDR-----FTESLHYYSTMFDSLEGGSSGG------GPSEVSSGAAAAPAAAGTD 526
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 317-276-24 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                 683 RLWKRLAGNGGMLSVMAPADRV-----RELMEPWAERMSVAAV--NGPASVTVAG---
                                                                                                                                                                                                                                                                          322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 GHE-RTGDPLWLGSLKSNIGHTQAAAGVAGVIKMVLALRHGELP------RTLH-- 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: FE
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les 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/804,227C
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TFVEMGPHPLLGAAIDEVAEAEGVHATALATLHRGSGGLDRFRSSVGAAFA 880
                                                                                                                                                      ----DARALEEFGGRLSAAGVLRWPLAGVDFAGHSPQVE-QFRAELLDTLGTVRPTAARL 785
                                                                                                                                                                                                                                                                   -----FTANQAILEAFAGCRRVHVVDFGIKQGMQ-WPALLQALALRPGGPPSFRLTGVGP 375
                                                                                                                                                                                                                                                                                                            RADVVQPTLFTMMVSLAALWESHGVRPAAVVGHSQGEIAAAHAAGALSLDDAARVIAERS 682
                                                                                                                                                                                                                                                                                                                                                                                       PVFVFPGQGSQWTGMGAELLDRAPVFRAKAEECARALAAHLDWSVL-DVLRDAPGAPPID 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSVVEAAPPVAAAANATPALPVVVVDTQEAGIRLVHALLACAEAVQQENLSAAEA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASTASSRIEWDAGAVELLDEAR-PWPRRAEGPRRAGISSFGISGTNAHLVIEEEPPA--- 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTDLSSWVE----SMLSELNAPPPPLPPAPQLNASTSSTVTGSGGYF---DLPPSVDS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYKVRASD----MADVAQKLEQLEMAMGMGGV-----GAGAAPDDSFATHLATDTVHYN 94
                                    TVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEGGSSGGGPSEVSSGAAAA 519
                                                                                                             EPFML-----QPEGEEDPNEEPEVIAVNSVFEMHRLLAQPGALEKVLGTVRAVRPRIV 468
                                                                                                                                                                                          PQPDETDALQQVG-----WKLA--QFA-HTIRVDFQYR------GLVAATLADL 415
                                                                                                                                                                                                                                                                                                                                                 -----QPDSSLLDAAFADLLHAH-----FYESCPYLKFAH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------RPEPEEAAQPPAPATTVLPLSAAGAR-----SLREQARRLAAHLAGHEE 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDAGGSGGGGGGGGSSEDKMMVSAAA-------GEGEEVDELLAAL 44
                                                                         -PFFSTVTAAAHEPEG------LDAAY-WYRNMREPVEFASTLRTL--LREGHR 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1580 amino acids
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N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                            ------LVKQIPLLAASQGGAMRKVAAYFGEALARRVFRFRP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%; Score 122; DB 2; Length 1580; 20.7%; Pred. No. 0.26;
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US-08-804-198-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.8%; Score 122; DB 2; Best Local Similarity 20.7%; Pred. No. 0.26; Matches 135; Conservative 78; Mismatches 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE IS80 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3885 FORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                  564 PVFVFPGQGSQWTGMGAELLDRAPVFRAKAEECARALAAHLDWSVL-DVLRDAPGAPPID 622
                                                                                                                                                                                          201 SSVVEAAPPVAAAANATPALPVVVVDTQEAGIRLVHALLACAEAVQQENLSAAEA-----
                                                                                                                                                                                                                                                                                      146 SSSIYALRPIPS-----PAGATAPADLSADSVRDPKRMRTGGSSTSSSSSSSSSIGGGAR 200
                                                                                                                                                                                                                                                                                                                                  407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 QD-GASNGLTAPSGPAQQRVIREALADAGLTPADVDAVEAHGTGTPLGDPIEAGALMATY 359
                                                                                                                                                                                                                                                                                                                                                                                                                       360 GHE-RTGDPLWLGSLKSNIGHTQAAAGVAGVIKMVLALRHGELP------RTLH-- 406
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                                                                                                                                                                                                                                                                                                                                                                           95 PTDLSSWVE-----SMLSELNAPPPPLPPAPQLNASTSSTVTGSGGYF---DLPPSVDS 145
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                                                                                                                                                                                                                                                                                                                                  ASTASSRIEWDAGAVELLDEAR-PWPRRAEGPRRAGISSFGISGTNAHLVIEEEPPA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDAGGSGGGGGGGGSSEDKMMVSAAA------GEGEEVDELLAAL 44
                                                                                                                                                       ITAADAARSAATTRAALSHRASVLADDRRA---LIDRLTALAEDRKDPGVTVGEAGSGRP
                                                                                                                                                                                                                                          -----RPEPEEAAQPPAPATTVLPLSAAGAR-----SLREQARRLAAHLAGHEE
-----QPDSSLLDAAFADLLHAH------FYESCPYLKFAH---
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Kuhstoss, Stuart A.
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CURRENT FILING DATE: 1999-10-28

EARLIER APPLICATION NUMBER: 60/120,254

EARLIER FILING DATE: 1999-02-16

EARLIER APPLICATION NUMBER: 60/106,100

EARLIER FILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 4150
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OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2
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Best Local Similarity
Matches 147; Conserv
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Patent No. 6251636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 30062-20029.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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                                          3357 --- DTFDADAVALSSLRRDEGGLDRFLTSLAEAFVQGVPVDWTHAFEGGRPRFVDLPTY-
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                                                                                                                                                                        163 APADLSADSVRDPKRMRTGGSSTSSSSSSSSLGGGARSSVVEAAPPVAAAANATPALPV
  279 GEALARRVFRFRPQPDSSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEAFAGCRRV 338
                                                                                    223 VVVDTQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPL--LAASQGGAMRKV--AAYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                14 GGGGM---GSSEDKM------MVSAAA------GEGEEVDELLAAL---GYKV
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                                                                                                                              -----TNLRETVRFQ------EAVEGLVAQGMGAFVECSPHPVLVPGITETL--
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Pred. No. 1
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; ORGANISM: Homo
US-08-922-635-22
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US-08-922-635-22
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LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: PILETZ, John
APPLICANT: IVANOV, Tina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/08922635A Patent No. 6033871
                                                                                                                                                                                                                                                                                                                                 Query Match 3.8%;
Best Local Similarity 20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/922,635A CURRENT FILING DATE: 1997-09-03 EARLIER APPLICATION NUMBER: 08/650,766 EARLIER FILING DATE: 1996-05-20 EARLIER APPLICATION NUMBER: 60/012,600 EARLIER FILING DATE: 1996-03-01 NUMBER OF SEQ. ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn
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744 ACVLLSTKAVYF--VLHDGLRRYFSEPLQDFWHQKNTDYNNSPFHISQCFVLKLSDLQSV
                                      267
                                                                                                                                                        624 VPAPAPAAASASGPAKTPAPAEASTSALVPEETPVEAPAPPPAEAPAQYPSEHLIQATSE
                                                                                                                                                                                                                                                                          121 QLNASTSSTVT-----GSGG-----YFDLPPSVDSSSSIYALRPIPSPAGATAPADLS 168
                      QGGAMRKVAAYFGEALARRVFRFRPQPDSSLLDAAFADLLHAHFYES-CPYLKFAHF-TA
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                                                                           ENQIPSHLPACPSLRHVASLRGSAIIELFHSSIAEVENEELRHLMWSSVVFYQTPGLEVT
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                                                                                                                  ----AGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAAS
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Pred. No. 0.2;
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GENERAL INFORMATION:

APPLICANT: Betlach, Mary C.

APPLICANT: Bothack, Sanjay Krishnakant

APPLICANT: McDaniel, Robert

APPLICANT: McDaniel, Robert

APPLICANT: Tang, Li

TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE

FILE REFERENCE: 30062-20029.00

CURRENT APPLICATION NUMBER: US/09/428,517

CURRENT FILING DATE: 1999-10-28

EARLIER APPLICATION NUMBER: 60/120,254

EARLIER FILING DATE: 1999-02-16

EARLIER FILING DATE: 1999-02-16

EARLIER FILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQ ID NO 3; LENGTH: 3816; TYPE: PRT
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-3
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US-09-428-517-3
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Best Local Similarity 20:7
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09428517 Patent No. 6251636
                                                                                                                                                                                                                                                                                               2311 RRVPVDYASHSAQMDQLRDELLEAL-----ADITPQHSSVPFFSTVTADWLDTTALDAG 2364
                                                                                                                                                                                                                                                                                                                                                                                                       2251 GGGGMYSVGLSAERVRTMLDTYGGRVSVAAVNGPSSTVVSGDVQALDELLAGCEREGVRA 2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1020 VPGGPARASQGREVQWQVFVPSAESREKLISLLARQWEALCGREL 1064
                                                                              2425 EGGLDRLLTSLAEAFVQGVPVDWTHAFEGMTPRTVDLPTYPFQRQHYWPKPAPAP---- 2479
                                                                                                                                                                                      2365 YWFTNLRETVRFQEAVEGLVAQGMGAFVECSPHPVLVPGIEQTLDALDQNAAVLGSLRRD 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 SGGGPSEVSSGAAA-----APAAAGTDQVMS-----EVYLGRQI 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        960 EFAKEPPQRDRYRLDDGRRVRDLDRVLMGYQTYPQALTLVFDDVQGHDLMGSVTLDHFGE 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 AVNSVFEMHRLLAQPGALEKVLGTVRAVRPRIVTVVEQEANHNSGTFLDRFTESLHY--- 492
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170 DSVRDPKRMRTGGSSTSSSSSSSSSSLGGGARSSVVEAAPPVAAAANATPALPVVVVDTQE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 NQAILE---AFAGCRRVHVVDFGIKQGMQWPALLQALALRPGGPPSFRLTGVGPPQPDET 381
                                                                                                                                                                                                                                                                                                                                                            49
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 GGGGM---GSSEDKM-------WVSAAA----------GEGEEVDELLAAL---GYKV 48
                                                                                                                                                                                                                                                                                                                                                 R-----ASDMADVAQKLEQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPT---DLS 99
                                                                                                                                    -GGYFDLPPS-----VDSSSSIYALRP----IPS-----PAGATAPADLSA 169
                                                                                                                                                                                                                                            SW------VESMLSE-LNA-----PPPPLPPAPQ--LNA-STSSTVTGS---- 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
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	; LENGTH: 1384 amino acid; TYPE: amino acid	
	CHARACTERISTICS:	
	; INFORMATION FOR SEQ ID NO: 11:	
	; TELEFAX: (213) 955-0440	
	; TELECOMMUNICATION INFORMATION:	
9/182	NUMBER: 229	
	; NAME: Warburg, Richard J. ; REGISTRATION NUMBER: 32,327	
. 6	Y/AGENT INFORMATION:	
UI	ICATION NUMBER: 60/031,675	
	Α.	
	136581ember 21,	
76, 255	NT APPLICATION DATA: LICATION NUMBER: US/08/976,	
2.0	ARE: FastSEQ for Windows 2.0	
DOS 5.0	P.C. DOS 5.	
	PE: storage	
1.44 Mb	. 44	
	90071-2066	
	TRY:	
	; CITY: Los Angeles	
ć	Suite 4700	
Ď.	; ADDRESSEE: Lyon & Lyon	
	CE ADDRES	
NES AND USES	OF INVENTION: KINASE GENES AND US	_
	, Gregory	
	AL INFORMATION:	
255	Sequence 11, Application US/0897625 Patent No. 6136581	
	RESULT 13 US-08-976-255-11	
VYLGRQICNVVACEGAE 548    ::	Qy 50% GGPSEVSSGAAAAAPAAGTDQVMSEVXLGRQICMVVACEGAE	
LARARGSAEHAMFRVEWVEEGSAADRCRGGA 280		
SGTFLDRFTESLHYYSTMFDSLEGGSS 506	Qy 454 EKVLGTVRAVRPRIVTVVEQEANHNSGTFLDRFTESLHYYSTMFDSLEGGS	
GATSLRVRVSPAGPDTVALALADPAGA 275	Db 2704 LGSFVEDPGQVYLPFLWSDVTLHATGATSLRVRVSPAGPDTVAL	
EPEVIAVNSVFEMHRLLAQPGAL 453	Qy 426EDPNE	
-GLHTAWRHGDDVYAEVALPEGTPADGYALHPALLDAAVQAVG 270	Db 2646 YARLVERGYTYGPSFQGLHTAWRHGDDVYAEVA	
TLADLEPFMLQPEGE 425	RGLVAA	
PGGTGAARPTEPAGVWPPAGAEPVALASDR 2	-AGFHRWTRHASGEVV-	
ALALRPGGPPSFRLTGVGPPQPDETDALQQVG 388	Qy 332 FAGCRRVHVVDFGIKQGMQWPALLQALALRPGGPPSFRLT	
	2576	
LDAAFADLLHAHFYESCPYLKFAHFTANQAILEA	272	
	) (	
FVELAVOAADRAGYDVLDELTLEAPLVLPDRGGIO 257	Db 2517 ISLR-THPWLADHEVLGSVLLPGTAFVELAVOAADRAGYDVLDELTLEAPLVLPDRGGIO	
CAEAVQQENLSAAEALVKQIPLLAASQGGAM 271	QY 230 AGIRLVHALLACAEAVQ	
-GANLGDVASVGLTAAGHPLLGAVVEMPDSDGLVL-TGQ 251	Db 2480GANLGDVASVGLT	

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Sequence 14, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
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                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        534 LGRQICNVVACEGAERTER 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 LAPAPCLYTPSWTETASSGG--DHPQAEPKLATEAEGTTGPRLPLPSVPSPSQEGA--PL 819
                                                                                                                                  STREET: LILLY CORPORTY: INDIANAPOLIS
STATE: IN
OPERATING SYSTEM:
                                                                                      COUNTRY: U:
ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GLLSGPAPQKRMGGPGTPRAPLRLALPGLPAALEGRPEEEEEDSEDSDESD 1182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGLPSTGQ-PS--EQVCLRPGVSGEAQGSGPGEVLPPLLQLEGSSPEPSTCPSGLVPEPP 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGIKQGMQWPALLQALALRPGG------PPSFRLTGVGP-----PQPD 379
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                                                                                                                                                                              LILLY CORPORATE CENTER
                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------AHFYESCPYLKFAHFTANQAILEAFAG----C--RRVHVVD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CEDLERKKK 1240
MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-804-227C-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 4545 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                                                               2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1731 GGLMGGLPVGGGMWSVGASESVVRGVVEGLGEWVSVAAVNGPRSVVLSGDVGVLESVVAS 1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 2101
                                                                                                                                                                                                                                                                                                                                                                                                   2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1911 MRRGRAEREVEEAALATVFTRDAGLDATALHTGSTGRRIDL-PTYPFQRDRYWLDPVRTA 1969
2236 GTGALGAQVARRLARSGAARLLLVGRRGAAGPGVGELVEELTALGSEVA-VEACDVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2014 AGHVLLLAPDEDTADSGL------APAIARELAVRGAEVHTVAVPVGTGREAAGDLL 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1851 LGDPGYWVRHAREAVRFADGVGVVRGLGVGTLVEVGPHGVLTGMAGECLGAGDDVVVVPA 1910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08, FILING DATE: February 21, CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44
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                                           SSGGGPSEVS----SGAA------AAPAAAGTDQVMSEV-YLGRQICNVVACEGAER 549
                                                                                                                                                                                                                                             QFAHTIRVDFQYRGLV----AATLADLEPFM--LQPEGEEDPNEEPEVIAVNSVFEMHRL 446
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                                                                                            ----APVPVPASARTVTTAPATAVGEDARNDTSDVVVPDDRWSSG-----TVLITG 2235
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RESULT 15 US-08-804-227C-8

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Sequence 8, Application US/08804227C Patent No. 5876991

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APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A
APPLICANT: Rosteck, Paul R., of
APPLICANT: Sutton, Kimberly L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION UNMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 317-276-2459 INFORMATION FOR SEQ ID NO: 8:
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TOPOLOGY: unknown
MOLECULE TYPE: peptide
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LENGTH: 4550 amino aci
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COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
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APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1856 LGDPGYWYRHAREAVRFADGYGYVRGLGYGTLVEYGPHGYLTGMAGECLGAGDDYYVVVPA 1915
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ZIP: 46285
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                                                                                             RAAGDGAARSTRVLWLAPAEPDAA--DAV-----
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LILLY CORPORATE CENTER
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Search completed: January 22, 2002, 16:24:19 Job time: 39 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	RESULT 1 AX005805 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
bread wheat Triticum aesti Eukaryota; Vir Spermatophyta; Pooideae; Trit 1 (bases 1 to Harberd,N.P. a Genetic contro Patent: WO 990 HARBERD NICHOL Locat 12 /orga	AX005805 Sequence : AX005805 AX005805		100. 100.	Que
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Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Harberd, N.P. and Peng, J.
Genetic control of plant growth and Patent: WO 9909174-A 3 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JIN
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AJ242531
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gibberellin respons
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Triticum aestivum
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Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1872)
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Nature 400 (6741),
99347734
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Flintham, J.E., Beales, J., Fish, L.J., Worland, A.J., P
Sudhakar, D., Christou, P., Snape, J. W., Gale, M.D. and
'Green revolution' genes encode mutant gibberellin r
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/translation="mkreyQDAGGSGGGGGGGGSSEDKMMVSAAAGEGEEVDELLAAL
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ATAPADLSADSVRDPKRMRTGGSSTSSSSSSSSSLGGGARSSVVEAAAPANATP
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/note="GAI ortholog"
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Query Match 88.0%; Best Local Similarity 99.9%; Matches 1871; Conservative

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Triticum aestivum
Eukaryota; Viridiplantae; Strept
Spermatophyta; Magnoliophyta; L:
Pooldeae; Triticeae; Triticum.
1 (bases 1 to 1768)
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Genetic control of plant growth and
Patent: WO 9909174-A 13 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JIN
Location/Qualifiers
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/ta; Liliopsida; Poales; Poaceae;
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 Spermatophyta; Magnollophyta; Liliopsida
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1746)
Harberd, N.P. and Peng, J.
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Sequence 57
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Triticum aestivum
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/db_xref="taxon:4565"
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT AB030956 LOCUS REFERENCE AUTHORS TITLE Ogawa,M., Rice gibbe

AB030956 Cryza sativa r Oryza sativa r AB030956 AB030956.1 GCOSGAI. mRNA bp mRNA
for OsGAI, complete cds.

30-MAR-2000

Oryza sativa (cultivar:Nipponbare) seedling cDNA to mRNA. Oryza sativa
Cryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. (sites) gibberellin-insensitive gene homolog,

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20179680
2 (bases 1 to 2500)
Sano,H., Ogawa,M. and Kusano,T.
Direct Submission
Submitted (09-AUG-1999) to the DDBJ/EMBL/GenBank databases.
Submitted (09-AUG-1999) to the DDBJ-EMBL/GenBank databases.
Mikihiro Ogawa, Nara Institute of Science and Technology, Plant Molecular Breeding; Takayama 8916-5, Ikoma, Nara 630-0101, Japan (E-mail:m-ogawa@bs.aist-nara.ac.jp, Tel:+81-743-72-5652,
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/product="orgal"
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/db_xref="taxon:4530".
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                                                   Submitted (03-MAY-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.or; On Apr 20, 2001 this sequence version replaced gi:13605985. Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                  Submitted (20-APR-2001) The Institute f Medical Center Dr, Rockville, MD 20850, 4 (bases 1 to 122497)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
3 B
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BAC OSJNBb0022E02
                                                                                                                                                                                                                                                                                                                                                                     for Genomic
0, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-2001 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                          Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      searches of the complete sequence against a pertide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu/GENSCAN.http://CCR-081.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotated as hypothetical proteins predicted by tRNAscan-SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes were identified by a combination of several methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://genemark.biology.gatech.edu/GeneMark/), and GeneSplicer
(Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dentified by repeatmasker (Arian Smit,
                                                                                                                                                                  GSDNTENGEDDTNGAAFVFSITAPAQPNQTTGVÄTVREEL"
complement(join(<5240...5517,5605...5644,6132...6212,
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11608...11698,12255...>12557))
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complement(5240...12557)
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/note="ST_D47656, AU088605 from this gene"
/note="105JNBb0022E02.2"
/note="105JNBb002E02.2"
/note="105JNB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
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SCRTRSSGTLEWTPVKTLALMAKVVVIDDGWSHSVSAFQKWAVLAENLAGSYFVAATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1271. .1579)
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/note="predicted by fgenesh"
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1386. .1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<1271.
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/sub_species="japonica"
/db_xref="taxon:4530"
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/gene="OSJNBb0022E02.11"
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/product="unknown protein"
                                                                                        11608. .11698,12255. .12388))
/gene="OSJNBb0022E02.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="OSJNBb0022E02.18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="OSJNBb0022E02.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="OSJNBb0022E02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
L. .122497
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GWTGDGSGYGRTGFHER NGEWYTCFCSWGWHGRSEVYFGKDRAAEERAACPFYROESC
YEGGGLFFFELLSDFCIKSVIHIGGSVDDEANVHISHCHLINFGLKSFLSSMCLIFKFS
IVKGSKCHSCYQSKOPRKPHKAAEERNLAPLELLHSDLCEMNGVLTKGGKRYFMTLLD
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TEHTHELVSEEDVSEAPRRSKRQRTAKSFGDDFTYYLVDDTPKSISEAYASPDADYWK
EAVRSEMDSILANGTWEVTERPYGCKFVGKTWFKKLREDASHGLIVHOMDVXTAFL
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QIIGGLMYLASATRDISFAVSKLSRFTSNFGDDHWRALERVMRYLKGTVELGLHTTG
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complement(12558...12580)
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ISWYELIAATTFTLLKISGDVGALGWWDLFINYGIAECFAFLVCTRWFNWAIKSGNW
GEASSSSAIRYRDWESGLLLPSLEDHBQERLCGLPDIGGHVMKIPLVIFQVLLCMRL
EGTPPSAQYIPIFALFSPLFTLQGAGVLFSLARLLEKVVLLLRNGPVSPNYLTISSKV
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<21271.
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/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(18822. .18858)
/rpt_family="(CAGGC)n"
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/note="similar to gag pol polyprotein |

GI:4234852 (Zea mays)"

join(14168 . 15023,15131 . 15274,15344

17887 . 18048,18262 . 18366)

/gene="OSJNBb0022E02.12"
                                                           /rpt_family="(TA)n"
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/rpt_family="AT_rich"
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TATVEAEWLRDLLMDLPVVEKPTCEKTIEVCQEIKKLRSYNVGLHPNSEKPGRSLHEG
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21271. .21576
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/note="predicted by fgenesh"
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aggctgccgcgcgcgcgcgcgcgcgcgcgacgcgacgccgcgcgctgccggtcg
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VCMYGKLGEMDNAKKAFRDATEKNIVTWNTLITSYATAGLCDEALDVLAQMEQIGGTV
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complement(23165..25551)
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/rpt_family="(GGAGAA)n"
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Pred. No. 1.7e-132;
0; Mismatches 251;
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tgggcaacgccgggttcgagaccgtccacctgggctccaatgcctacaagcaggcgagca
                                                                    CGTGCGAGGGCGCGGAGCGCACGGAGCGCCACGAGACGCTGGGGCAGTGGCGCAACCGCC
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AUTHORS
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Harberd,N.P. and Peng,J.

Genetic control of plant growth and de Patent: WO 9909174-A 15 25-FEB-1999;

HARBERD NICHOLAS PAUL (GB); PENG JINEC Location/Qualifiers ce 1. 2255
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                                                                                      cgccgccgccctcccgccgcccgcagctc----aacgcctccacctcctccaccg
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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/db_xref="taxon:4577"
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Pred. No. 4.8e-129;
0; Mismatches 230;
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Direct Submission
Submitted (25-MAY-1999) Richards D.E., Molecular Gesting the Colney Lane, NR4 7UJ, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                      Nature 400
99347734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                        Peng, J., Richards, D.E., Hartley, N.M., Murphy, G.P., D
Flintham, J.E., Beales, J., Fish, L.J., Morland, A.J., P
Sudhakar, D., Christou, P., Snape, J. W., Gale, M.D. and
'Green revolution' genes encode mutant gibberellin r
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AJ242530
AJ242530.1 GI:5640154
D8 gene; gibberellin response
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                                            LGGSGFAPVHLGSNAYKQASTLLALFAGGDGYRVEEKDGCLTLGWHTRPLIATSAWRV
AAAAAP"
1 684 c 655 g 283 t
                                                                                                                                                                                                                                           /gene="d8"
1. .>1890
                                                                                                                                                                   /product="gibberellin response
/protein_id="CAB51557.1"
/db_xref="GI:5640155"
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/note="GAI ortholog"
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Pelica, F.,
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Query Match 61.6%; Best Local Similarity 84.7%; Matches 1611; Conservative

829 ggcggcgatgcgcaaggtcgccgcctacttcggcgaggccctcgccgccgcgcgtcttc 888	769 gagaacctctccgcgcgcgcgcgcgcgcgcgcgtcgtcggcggtcgtc	8 gegetgeggecegatecectececeggeeggegegaeggeggeggeeggeeggeeggeeg	6 gacctgtcgtcttgggtcgagagcatgctgtcggagctcaacgcgccgccgcccctc 3	139 gacgagettgctggcggcgctcgggtacaaggtgcgcgcctccgacatggcggacgtggcg 198	ery Match 61.6%; Score 1309.4; DB 8; Length 1890; st Local Similarity 84.7%; Pred. No. 3.2e-128; tches 1611; Conservative 0; Mismatches 226; Indels 66; Gaps 10; 28 atgaagcgggagtaccaggacggcgggagggagggggggg
RESULT 10 AF377646 AF377646 AF377646 AF377646 AF377646 DEFINITION Tripsacum dactyloides gibberellin response modulator gene, partial cds. ACCESSION AF377646 VERSION KEYWORDS SOURCE ORGANISM Tripsacum dactyloides Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Db 1714 TTCGCGCCCGTGCACCTGGGCTCCAATGCCTACAAGCAGGCAG		Oy 1509 gggccgggcccggggagagytcctgggaaggtcctggggacggggacggggacggggacaggaccaggaccaggaccaggaccaggaccaggaccaggaccaggaccaggaccaggaccaggaccaggaccaggaccaggaccaggaccagacagaccagacagacagaccagacagacagacagacagacagacagacagacagacagacagacagacagacagacagacagacagacagacagaaga	1189 GCTGGAAACTTGCCCAGTTCGCGCACACCATCCGTGGACTTCCAGTACCGTGGCCTC  1249 gtcgccgccacgctcgcggacctggagccgttcatgctgcagccggagggag	1009 atccts

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           acgccgccttcgccgacctcctccacgcgcacttctacgagtcctgcccctacctcaagt
                                                             agatacccttgctggccgcgtcccagggccgcgcgatgcgcaaggtcgccgcctacttcg
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                                                 AGATCCCCATGCTGGCCTCGTCGCAGGGCGGCGCCATGCGCAAGGTCGCCGCCCTACTTCG
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ACGCCGCCTTCGCCGACCTCCTGCACGCGCACTTCTACGAGTCCTGCCCCCTACCTGAAGT
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Patterns of DNA sequence
(Zea mays ssp. mays L.)

Proc. Natl. Acad. Sci. U.
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309 c 259 g 126 t
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 620.2; DB Pred. No. 3e-56;
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Submitted (07-MAY-2001) Ecology
University of California, Irvine
92697-2525, USA
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Patterns of DNA sequence polymorphism along
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/codon_start=3
/product="gibberellin response modulator"
/protein_id="AAK59901.1"
/protein_id="AAK59901.1"
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MLASSOGGAMRKVAAYFGEALARRVYRFRPPPDSSLLDAAFADLLHAHFYESCPYLKF
                                                                                                                                                           /sub_species="mays"
/db_xref="taxon:4578"
/chromosome="1"
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/cultivar="Serrano"
/isolate="GUA14"
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                                                                                                                                              /country="Guatemala"
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Pred. No. 6.4e-56;
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                                                                    tggcgtgcgcggaggccgtgcagcaggagaacctctccgccgcggaggcgctggtgaagc
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Submitted (07-MAY-2001) Ecology and Evolutionary
University of California, Irvine, 321 Steinhaus,
92697-2525, USA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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Tenaillon,M.I., Sawkins,M.C., Long,A.D., Gaut,R.L., Doebley,J.F.
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AHFTANQAILEAFAGCRRVHVVDFGIKQGMQWPDSSLLDAAFADLLHAFFYESCPYLKF
AHFTANQAILEAFAGCRRVHVVDFGIKQGMQWPDALLQALALRPGGPPSFRLTGYGPPQ
PDETTANQAICAGGAHTIRVDFQYRGLVAATLADLEPFMLQPEGD"
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/cultivar="Zapalote Chico"
/isolate="OAX70"
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AF377627.1 GI
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Zea mays
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University of California,
92697-2525, USA
                                                                                                                                                                and Gaut, B.S.
                                                                                                                                                                           Tenaillon, M.I.,
                                                                                                                                                                                                            and Gaut, B.S.
Patterns of DNA sequence
(Zea mays ssp. mays L.)
Proc. Natl. Acad. Sci. U.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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 /product="gibberellin
                     /country="Mexico: northern"
                                                                /isolate="CHH160"
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120 628 60 571

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Score 617; DB 8; I Pred. No. 6.4e-56; 0; Mismatches 90; Length Indels 1 800 9; Gaps Š

В

781

TGCTGCAACCGGAGGGCGA

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BASE COUNT
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PUBMED
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Best Local Similarity 87.6
Matches 700; Conservative
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cgctgccggtcgtcgtcgtcgacacgcaggaggccgggattcggctggtgcacgcgctgc
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AF377633
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
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gene, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /country="Mexico: southern"
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/cultivar="Bolita"
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0; Mismatches 90;
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              Submitted (07-MAY-2001) Educated University of California, 92697-2525, USA
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Eukaryota; Viridiplantae;
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                                                         Direct Submission
                                                                      and Gaut, B.S.
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                                                                                Tenaillon, M.I., Sawkins, M.
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Location/Qualifiers
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                             Irvine,
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                                                                                  Gaut, R.L.,
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                             nd Evolutionary 321 Steinhaus,
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                                                                                  Long, A.D.,
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acgagaccgacgcctgcagcaggtgggctggaagctcgcccagttcgcgcacaccatcc
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PDETDALQQVGWKLAQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGD"
a 306 c 263 g 127 t
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A. thaliana transc	AAD06646	22		17.9	380.2	9
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Arabidopsis thalia	AAC45745	21		18.0	382	7
Rice EST D39460 se	AAX36277	20		19.8	420.4	6
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Consensus cDNA seq	AAX36285	20		64.9	1379.8	4
Wheat Rht clone C1	AAX36278	20		70.7	1502.4	w
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## ALIGNMENTS

RESULT AAX36279 16-JUL-1999 (first entry) AAX36279; AAX36279 standard; DNA; 2125 ם ВP

Wheat Rht clone 5al genomic sequence.

paclobutrazol; ss. Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;

Triticum aestivum.

W09909174-A1.

25-FEB-1999.

07-AUG-1998; 98WO-GB02383

13-AUG-1997; 97GB-0017192.

(PLAN-) PLANT BIOSCIENCE LTD

Harberd NP, Peng J, Richards DE;

WPI; 1999-181040/15. P-PSDB; AAY02540.

New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Trilicum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which hare resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents
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Query Match Best Local S Matches 1503

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Similarity

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                                          The specification describes polypeptides encoded by the Rht gene (and content of the plant. When expressed in Triticum Aestivum, inhibit content of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-in-insensitive. Taller plants waild-type, the dwarfing out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as pacibutrazol, e.g. to allow use of a gibberellin biosynthesis, such as pacibutrazol, dwarf but let crop plants grow tall. The present sequence represents the wheat Rht clone C15-1 cDNA sequence.
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New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype

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The specification describes polypeptides encoded by the Rht gene (and cits homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the maize lal genomic clone sequence.
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                                                                                                          cgtcgtcatcctcctcctcgtcgtctctcggtggg---gcgccaggagctctgtggtgg
                                                                                                                                                                    acccgtccacggactcggcgcgggagcccaagcggatgaggactggcggcggcagcacgt 770
                                                                                                                                                                                                                                                         ccagcagtacctacgctctgaagccgatcccctcgccg---gtggcggcgccgtcggccg
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aagctgcgccgccggcgacgcaagcatccgcggcggccaacgggcccgcggtgccggtgg
                                                                                  cgtcctcctcctcgtcgtcatccatggatggcggtcgcactaggagctccgtggtcg
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84.6%;
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Pred. No. 2.6e-172;
0; Mismatches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 66;
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δ 뫄 Qy Qy

В QΥ В Qγ 밁 δ 망 Ş

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1715 1896 1775	83	1595 1776	1535 1728	1475 1668	1415 1608	1355 1548	1295 1491	1235 1431	1175 1371	1115 1311	1055 1251	995 1191	935 1131	875 1071	815 1011	755 951	695 891
tgggcaacgccgggttcgagaccgtccacctgggctccaatgcctacaagcaggcgagca 1774	cctgcgaggggggggggcgcacagagcgccacgagacgctgggccagtggcgggaaccggc 171	ccggcacggaccaggtcatgtccgaggtgtacctcggccggc	gcageteeggeggeeggeecateegaagteteateggggggetgetgetgetgeteetgeegeeg 1594	i tygaccycttcaccyaytctctycactactactccaccatyttcyattccctcyaygycy 1534 	tgcggcccaggatcgtcaccgtggtggagcaggaggcgaatcacaactccggcacattcc 1474	tgcaccggctgctcgcgcagcccggcgccctggagaaaggtcctgggcaccgtgcgcgccg 1414	agggcgaggaagacccgaacgaggagcccgaggtaatcgccgtcaactcagtcttcgaga 1354 	agtaccgcggcctcgtcgccgccacgctcgcggacctggagccgttcatgctgcagccgg 1294	cectgeageaggtgggetggaagetegeeeagttegegeacaceateegegtegaettee 1234	geggeeeteeetegtteegeeteaeeggegteggeeeeegeageeggaegagaeegaeg 1174	teggeatcaagcaggggatgcagtggccegcacttctccaggccctcgccctccgtcccg 1114	ccgccaaccaggccatcctggaggcgttcgccggctgccgcgcgcg	ccgacctcctccacgogcacttctacgagtcctgcccctacctcaagttcgcgcacttca 994	cocycogcytottccycttccyccogcagccygacagctccctcctcgacyccyccttcy 934	tggccgcgtcccagggcggcgcgatgcgcaaggtcgccgcctacttcggcgaggccctcg 874	aggccgtgcagcaggagaacctctccgccgcggaggcgctggtgaagcagatacccttgc 814	tcgtggtcgacacgcaggaggccgggattcggctggtgcacgcgctgctggcgtgcgcgg 754

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RESULT
AAX36277
ID AAX3
XX AAX3
XX AAX3
XX AAX3
XX Rht
KW Rht
KW Rht
KW anta
KW PAC1
XX O172
XX V099
XX 13-A
XX 13-A
XX 11-A
XX PT Hart
XX PT Hart
XX PT PTON
PT PTON
PT PTON
PT PTON
PT PTON
PT ANTE
XX Clad

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes polypeptides encoded by the Rht gene (and C its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by CC globerellin. This growth inhibition is antagonised by CC globerellin. The products can be used to provide Rht expression in CC plants, conferring a dwarf phenotype on a plant which is correctable by treatment with globerellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being globerellin-insensitive. Taller plants CC may be made by knocking out Rht or the relevant homologous gene in CC the plant of interest. Plants may be made which are resistant to CC compounds which inhibit globerellin blosynthesis, such as paclobutrazol, CC e.g. to allow use of a globerellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents contact the plants grow tall. The present sequence represents the force where the contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; rice; expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antagonised by gibberellin, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 770 BP; 104 A; 252 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harberd NP, Peng J,
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                                                                                                                      aagcgggagtaccaggacgccggagggagcggcggcggcggtggcggcatgggctcgtcc
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t Rht gene.
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                                                                                                                                                                                                                                Score 420.4; DB 2
Pred. No. 9.1e-50;
0; Mismatches 146
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RESULT
AAC45745
ID AAC4
XX AAC4
AC AAC4
XX Arab
XX Hybr
KW Prott
KW Prott
KW meta
XX Arab
XX Arab
XX Arab
XX EP10
XX Arab
XX EP10
XX O6-S
YC O5-F
PR 05-F
PR 05-F
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 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                  EP1033405-A2
                                                                                                                        Arabidopsis thaliana
                                                                                                                                                   metabolic
                                                                                                                                                             Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
                                                                                                                                                                                                 Arabidopsis thaliana DNA fragment SEQ
                                                                                                                                                                                                                                                                          AAC45745 standard; DNA; 1602
                                                                          06-SEP-2000
                                                                                                                                                                                                                         18-OCT-2000
                                                 25-FEB-2000;
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                   ttggtccaccggcaccggataatttcgattatcttcatgaagttgggtgtaagctggctc
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Pred. No. 1.4e-44;
0; Mismatches 415;
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                                                                                                        dwarf phenotype; lodging resistance; increased yield
flowering regulation; bolting inhibition; spinach;
antibody; identification; probe; primer; antisense;
expression regulation; co-suppression; rice;
                                                                                                                                                                                                                                                                                             1568
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                                                                                                                                                Gibberellin insensitivity; gai; plant growth inhibition;
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           12-FEB-1997;
                                14-AUG-1997.
                                                    WO9729123-A2
                                                                         Arabidopsis
                                                                                                                                                                       Arabidopsis thaliana gibberellin insensitivty
                                                                                                                                                                                              19-MAR-1998
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                                                                                                disease
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          97WO-GB00390
                                                                                                resistance;
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Best Local Similarity
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DB; AAW30792.
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metabolism; ss.
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Location/Qualifiers 196..1794

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germination rates of plants, photosynthesis, "glyoxylate metabolism," respiration, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, pigmentation, colling the metabolism, it is towering and senescence of plants and for modifying sink-source relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, onion, papaya, peas, peapers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.

The present sequence is an Arabidopsis thallana transcription factor
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 736; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-1999;
17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aspects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 72-74; 151pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factors which may be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tors which may be used to modify phenotype associated with a plant's ar sensing characteristics and increasing yield when their expression el is altered. Sugars are central regulatory molecules that control ects of physiology, metabolism and development. Therefore the cDNAs proteins of the invention are useful for modifying the growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patent relates to polynucleotides
                                                                                                                          ccgcggccaacgcgacgcccgcgttgccggttcgttggttcgacacgcaggaggccggga
ccgcggaggcgctggtgaagcagatacccttgctggccgcgtcccagggcggcgcgatgc
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Samaha R;
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ADAM L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIECHMANN J
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RESULT
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17-NOV-1999;
17-APR-2000;
22-AUG-2000;
                  such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugar came, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, egyplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. Transcription factors are key controlling elements of biological pathways and altering expression levels of lor more transcription factors can change entire biological pathways in an organism. Therefore manipulating transcription factor levels in plants offers great potential in agricultural blotechnology for modifying a plant's traits. Transcription factor cDNA
                                                                                                                                                        The present sequence is Arabidopsis thaliana transcription factor, G308 CDNA, a homologue of G307. The transcription factor is used for altering a plant's blochemical characteristics. The transcription factor may be used to alter the structure and developmental characteristics of plants
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The present sequence encodes a wild type plant protein of the GRAS family. The specification describes a mutant allele of the BZH gene, which contains a G1695A mutation resulting in the mutation E546K in the protein GRAS proteins are transcription factors implicated in regulation of the response to gibberellins and thus in control of morphogenesis and plant development. The mutant GRAS protein is used to produce dwarf plants, specifically crucifers. Dwarf plants may be sown earlier (increasing nitrate accumulation without risking excessive stem growth during winter), and have better resistance to cold and lodging. They are also easier to harvest and allow for better
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                     The present sequence encodes a mutant plant protein of the GRAS family. The mutant allele of the BZH gene contains a G1695A mutation resulting in the mutation E546K in the protein. GRAS proteins are transcription factors implicated in regulation of the response to gibberellins and thus in control of morphogenesis and plant development. The mutant GRAS protein is used to produce dwarf plants, specifically crucifers. Dwarf plants may be sown earlier (increasing nitrate accumulation without risking excessive stem growth during winter), and have better resistance to cold and lodging. They are also easier to harvest and allow for better monitoring of the crop.
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Query Match Best Local Similarity

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                                                                                                                                                                                     The specification describes polypeptides encoded by the Rht gene (and clist homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by glbberellin. This products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with glbberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being glbberellin-insensitive. Taller plants waid-type, the dwarfing being glbberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit glbberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a glbberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the wheat rht-10 allele.
Query Match
Best Local S
Matches 416
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Score 367; DB 20;
Pred. No. 1.9e-42;
0; Mismatches 0
                                                                                                                                         129
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                                                                                                                                         <u>ი</u>
                                                                                                                                         60 T; 0 other;
                                                       DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heat; growth inhibition;
gibberellin biosynthesis;
  0
                                                    Length 416;
  Indels
  39;
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RESULT 1
AAX36269
ID AAX3
AC AAX3
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AC DNA
XX Rht
KW Anta
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XX 13-1
PF 07-1
XX 13-1
PR 11-1
XX WPI
PX WPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           кли gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; ss.
                                                                                                                                                         New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                   WPI; 1999-181040/15.
                                                                                                                                                                                                                                                                                                Harberd
                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum
                                                                                                                                                                                                                                                                                                                                            (PLAN-) PLANT BIOSCIENCE LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence obtained after sequencing wheat Rht clone 5al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1999
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                                                                                                              English.
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in

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ARESULT 1
AAT91938
ID AAT99
XX AAT9
AC AAT9
XX AAT9
DT 19-M
DT 19-M
CONTROL ATAB
XX G1bb
KW G1bb
KW G1bb
KW G1bb
KW G1bb
KW G1bb
KW G1bb
XX G1
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Best Local Similarity
Matches 365; Conserv
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                                                                                                                                                                                                                                                                                       dwarf phenotype; lodging resistance; increased yield; flowering regulation; bolting inhibition; spinach; le antibody; identification; probe; primer; antisense; sexpression regulation; co-suppression; rice;
                                                                                                                                                                                                                                                                                                                                                                                                    Gibberellin insensitivity; gai-dl; plant growth inhibition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana gibberellin insensitivty gene gai-d1.
     12-FEB-1996;
                                                      12-FEB-1997;
                                                                                                          14-AUG-1997.
                                                                                                                                                                                                                  Arabidopsis thaliana
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                                                                                                                                                                                                                                                                      disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                                                      resistance; ss.
     96GB-0002796
                                                      97WO-GB00390.
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95.5%;
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Pred. No. 2.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                764
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latter for increased resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the vegetative state until treated with GA, useful to inhibit bolting in spinach and lettuce. GAI-dl can be used to raise specific antibodies for identifying homologous proteins or genes in other species. gai-dl fragments can also be used as probes or primers to identify and clone related sequences, or in the preparation of antisense or sense expression regulating (or-suppressing) sequences. Rice plants that express Gal may be resistant to Bakane disease. Manipulation of gai-dl and GAI-dl may be resistant to the telegree of dwarfism and GA sensitivity to particular crops
                                                                                                                                                                                                                                                                                     The present sequence encodes the Arabidopsis thaliana gibberellin insensitivity (gai-dl) gene product (GAI-dl), the expression of which inhibits plant growth. However the inhibition is antagonised by gibberellin (GA), while gai expression confers a dwarf phenoty; that is insensitive to GA. Manipulating gai-dl and GAI-dl expression can produce tall or dwarf plants, particularly the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding gibberellin inhibitor GAI and related antisense sequences - used to create tall, or particularly, plants, especially crops such as maize, rice and wheat.
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                                                                                                                                                                                                                                                                                                                                 phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dwarf
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Sequence 1643 BP; 405 A; 359 ü 423 **G**; 456 T; 0 other;

Local Similarity

16.6%;

Score 351.8; DB 1 Pred. No. 1.9e-40;

DB 18;

Length

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밁 δÃ 밁 Ş 밁 Ş 밁 δÃ 밁 Š 밁 Š В QΥ B δÃ Matches 701; 1142 536 662 656 902 ccgcggaggcgctggtgaagcagatacccttgctggccgcgtccccagggcggcgcgatgc ttcggctggtgcacgcgctgctggcgtgcgcggagggccgtgcagcaggaggaacctctccg ccgcggccaacgcgacgcccgcgctgccggtcgtcgtggtcgacacgcaggaggccggga gcgtcggcccccgcagccggacgagaccgacgccctgcagcaggtgggctggaagctcg cggcgcttatgcaggctcttgcgcttcgacctggtggtcctcctgttttccggttaaccg ttcaagggaagaaaagagttcatgtcattgatttctctatgagtcaaggtcttcaatggc tcgccggctgccgcgtgcacgtcgtcgacttcggcatcaagcaggggatgcagtggc agacttgtccttatctcaagttcgctcacttcacggcgaatcaagcgattctcgaagctt agtcctgcccctacctcaagttcgcgcacttcaccgccaaccaggccatcctggaggcgt cgcag---agcoggacagctccctcctcgacgcccttctgccgacctcctccacgcgccacttctacg tggcggaagctctggtgaagcaaatcggattcttagctgtttctcaaatcggagctatga tgcgtctcgttcacgcgcttttggcttgcgctgaagctgttcagaaggagaatctgactg ccacagcgacggctgagtcaactcggcatgttgtcctggttgactcgcaggagaacggtg Conservative agtccaatcgaccactctctctccgatactctttagatgcacttctacg 0; Mismatches 407; Indels 75; Gaps 1009 1081 1021 829 775 901 781 949 889 961 655

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Search completed: January 23, 2002, 02:37:26 Job time: 5950 sec

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   563.8

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BF588097 FM1_37_F0
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BF618807 HVSMEC000
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BE414891 MWL001.H0
B1417150 949053608
BF268018 HV_CEa001
                                                                                                                                         Description
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FEATURES Sour	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BG308975 LOCUS DEFINITION		8 8 8 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	C 	13 14 15 16 17 18 18 20 21 22 23 24
100 Jordan Hall, Tel: 864 655 728 Fax: 864 656 429 Email: rwing@cle Seq primer: AATT High quality seg High quality set Locatic 1778 ce /organi/cultiv	Development of a for barley genomi Unpublished (2000 Contact: Wing RA Clemson Universit	; Triticeae 1 (bases 1 Wing,R., Cl ,Y., Anderso ,T., Saski, Wood,T.	BG308975.1 EST. barley. hordeum vulue Eukaryota; Spermatophy			88.8 8.6 70 8.3 4 4 4 3 7 4 4 3 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7	10.5 10.5 10.3 10.3 10.2 10.0 10.0 10.0 10.0 10.0 10.0 10.0	307.4 14.5 527 284.2 13.4 596 273.4 12.9 524 263.8 12.2 543 257.4 12.1 579 256.2 11.9 475 251.4 11.8 658 244.3 11.4 977 242.2 11.4 268
Clemson, SC 29634, USA 18 23 28 28 29 29 20 20 20 20 20 20 20 20 20 20 20 20 20	genetically and physically self-	se,R., Kernodl	; Streptophyta; hyta; Liliopsida	bp mRNA. EST rdeum vulgare seedling shoot ated and unstressed) Hordeum RNA sequence.	ALIGNMENTS			10 BE595338 10 AU065169 10 BE329503 11 BG043071 11 BG155663 10 AW704479 10 AU222715 10 BE364489 11 BF587541 10 BE196286 11 BF597541 11 BF587541
	anchored EST resource	Begum,D., Frisch,D., Yu e,S., Palmer,M., Rambo Choi,D.W., Main,D. and	Embryophyta; Tracheophyta; ; Poales; Poaceae; Pooideae	22-FEB-2001 EST library vulgare cDNA clone		word w C 0101 - w w w	0110000	BE595338 PI1_48 Gl AU065169 AU065169 BE329503 so66b12 y BG043071 st91h01 y BGL5563 saa64a06 y AW704479 sk53e12 y AU222715 AU222715 BE364489 PI1_14 F0 BF587541 FM1_37_F0 A1665907 606003E05 BE196286 HVSMEh009 BF201178 WHE0986_A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4513"
/clone="HVSMEC0001C18f"
/clone_11b="Hordeum vulgare seedling
/CDNA0003 (Etiolated and unstressed)
/tissue_type="Seedling shoot"
/lab_bost="TJC121"
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                                      accgcttcaccgagtctctgcactactactccaccatgttcgattccctcgagggcggca 1537
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gctccggcggcggcccatccgaagtctcatcgggggctgctgctgctcctgccgccgccg 1597
                                                                                                                                         ggcccaggatcgtcaccgtggtggagcaggaggcgaatcacaactccggcacattcctgg
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poolde
; Triticeae; Hordeum.
1 (bases 1 to 597)
Wing,R., Close, T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Ramb
,Y., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVSMEC0018M11f Hordeum vulgare seedling shoot HVcDNA0003 (Etiolated and unstressed) Hordeum HVSMEC0018M11f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000) on Dec 18, 2000 this sequence version replaced gi:11883915.
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Clemson Hall, Clemson,
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High quality sequence stop: 564.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Hordeum vulgare seedling shoot EST library
HVcDNA0003 (Etiolated and unstressed)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
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/clone="HVSMEc0018M11f"
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/cultivar="Morex"
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High quality sequence start: 27
High quality sequence stop: 611.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
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HVSMEF0003G24f Hordeum vulgare seedling root EST library HVcD
(etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEF0003G24f, mRNA sequence.
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19,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rami
,, Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. at
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                                  order
                                                /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Fo
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
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HVcDNA0007 (etiolated and unstressed)
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/lab_host="TJC121"
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                                       Sorghum propinguum.
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The University of Georgia
Plant Sciences Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
Sequence Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Cordonnier-Pratt MM
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/note="Organ: Floral-Induced meristems; Vector:
/note="Organ: Floral-Induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
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/db_xref="taxon:132711"
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gcacattcctggaccgcttcaccgagtctctgcactactactccaccatgttcgattccc
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1 (bases 1 to 593)
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Plate: 606074 row: G colu
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Tel: 650 723 2227
Fax: 650 725 8221
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; Site_2: XhoI; Mixed ear tissue
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/dev_stage="ear length from 0.5 cm
/lab_host="XLOLR (Stratagene)"
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/cultivar="Ohio43"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                         Stanford University
855 California Ave, F
Tel: 650 723 2227
Fax: 650 725 8221
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Zea mays
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Contact: Walbot V
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606052F10.x2 606 - Ear tissue
mays cDNA, mRNA sequence.
A1770444
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                                                              Ø
                                                                                                                                         /organism="Zea mays"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/clone_llb="606 - Ear
                                                                                        /dev_stage="ear length from 0.5 cm
/lab_host="XIOLR (Stratagene)"
/note="Organ: immature ear; Vector:
                                                                                                                                                                                           6052 row: F column Location/Qualifiers
                                                                                                                       /tissue_type="mixed"
                                                                                Site_2:
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          19.8%;
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Score 421.2; DB 10;
Pred. No. 7.8e-49;
D; Mismatches 68;
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                                                                                                                                                                                                                                                      propinguum
BF655617
        Seq primer: JEN REV High quality sequen
                             below Phred quality is 20.
                                                 Email: mmpratt@uga.edu
Sequences have been tr
                                                                     Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                               Unpublished (2000)
                                                                                                                                          An EST database from
                                                                                                                                                                                                               Sorghum propinguum.
Sorghum propinguum
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                                                                                                                                     Department of Botany
The University of Georgia
Plant_Sciences Building,
                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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                                                                                                                                                                                            Contact: Cordonnier-Pratt
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                                                 trimmed 16. The
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stop:
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HVSMEC0007P09f Hordeum vulgare seedling shoot EST library
HVCDNA0003 (Eticlated and unstressed) Hordeum vulgare cDNI
HVSMEC0007P09f, mRNA sequence.
Wing,R., Close,T.J., Kleinhofs,A., Wi
                                    Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida
; Triticeae; Hordeum.
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/db_xref="taxon:132711"
/clone_lib="Floral-Induced Meristem 1 (FM1)"
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91.4%;
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 Wise, R., Begum, ., Kernodle, S.,
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Fax: 864 656 4293
Email: rwing@clemson.edu
Emair: rwing@clemson.edu
Emair: rwing@clemson.edu
High quality sequence start: 2
High quality sequence stop: 405.
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Clemson University
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib-"Hordeum vulgare seedling shoot
HYCDNA0003 (Etiolated and unstressed)"
/tissue_type-"Seedling shoot"
/lab_host-"TJC121"
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ggcctcgtcgccgccacgctcgcggacctggagccgttcatgctgcagccggagggggag 1302
                                                     caggtgggctggaagctcgccagttcgcgcacaccatccgcgtcgacttccagtaccgc 1242
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                                      CAGGTGGGCTGGAAACTTGCTCAGTTCGCGCACACCATCCGCGTCGACTTCCAGTATCGT
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BI098997
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IP1_36_A11.b1_A002
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/note="Organ: Developing preanthesis pannicles; vpBluescript II SK(-) from Lambda Zap II; Site_1:
Site_2: EcoRI; The library was made from poly-a relationing vector lambda ZAP II. Clones to be seque prepared by mass excision."

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/cultivar="BTx623"
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CATCCTGGAGGCGTTCGCCGGCTGCCGCGTGCACGTCGTCGACTTCGGCATCAAGCA
                                                                CGCGCACTTCTACGAGTCCTGCCCCTACCTCAAGTTCGCCCCACTTCACCGNCAACCAGGC
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International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Warburton M
Applied Biotechnology Center, CIMMYT
Apdo. Postal 6-641, 06600 Mexico DF I
Tel: 52-5-7269091 ext 1381
Fax: 52-5-726758/59
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Triticum aestivum
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cDNA clone MWL001.H03,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mwarburton@cgnet.com
International Triticeae EST Cooperative
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/dev_stage="8 day old"
/note="vector: pYES2 (
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/clone="MWL001.H03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Walbot V
Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays
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BI417150
                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 949053 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California Ave, Palo Alto, CA 94304, USA
            //dev_Stage="4 stages from 3-13 days after imbibing"
//lab_host="E. coli XLOLR"
//note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcoR1; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing-includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
                  62
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                                                                                                                                                                                                                                                                                         meristem"
                                                                                                                                                                                                                                                                                                                         Moose"
                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4577"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/cultivar="W64A"
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Query Match

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Length 481;

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BF268018
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rami
T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. au
                                                                                                                                                                                                                                                                  Clemson University
100 Jordan Hall, Clemson,
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                                                                                                                              Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 587.
                                                                                                                                                                                                               Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                              Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
On Nov 17, 2000 th
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/organism="Hordeum vulgare"
/cultivar="CI16155 (Mla13)"
/db_xref="taxon:4513"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTAGATCTCCCGCGCTCTGTCGACTACTCCAGCAGAAACCTACGCCCTGGGCCCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTCTCCTCCTGGGACGAGGAGCATGCTGGCCGAGCTCAACGCGCCTCCGACGGCCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410;
An EST database from Sorgh
Unpublished (2000)
Contact: Cordonnier-Pratt
                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 527)
                                                                                                                                 sorghum bicolor
                                                                                                                                                                                                         BE595338 527 N
PI1_48_G12.b1_A002
mRNA sequence.
                                                                                                                                                                  EST
                                                          Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                              BE595338.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library HVcDNA0004 (Erysiphe infected /tissue_type="seedling green leaf" /lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="HV_CEa0019J17f"
/clone_lib="Hordeum vulgare seedling green leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%;
79.5%;
                                                                                                                                                                               GI:9850411
                                                                                                                                                                                                                    bp mĸwa
)2 Pathogen
                              Sorghum:
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Pred. No. 1.7e-33;
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                                                                                                                                                                                                                         induced
                              pathogen-induced
                                                          Dean,R.,
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                              plants
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CCATGCTGGCCTCGCCAGGGCGGTGCCATGCGCAAGGTCGCCGCCTACTTCGGCGAGG

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Best Local Similarity
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                                                                                                                                                                                                                                                                                        GCACGTCGTCTTCGTCCTCGTCGTCATCCATGGATGGCGGCCGCACTAGGAGCTCCG
                                                                           gcgcggaggccgtgcagcaggagaacctctccgccgcggaggcgctggtgaagcagatac
                                                                                                                                                       cggtcgtcgtggtcgacacgcaggaggccgggattcggctggtgcacgcgctgctggcgt 748
                                                                                                                                                                                                                                    tggtggaggctgcccggccggtc-----gcggccgcggccaacgcgacgcccgcgctgc
                                                                                                                                                                                                                                                                                                          gcacctcgtcgtcatcctcctcctcgtcgtctctcggtgggg---gcgccaggagctctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGCGGAGGCCGTGCAGCAGGAGAACTTCTCTGCGGCGGACGCGCTGGTCAAGCAGATCC
                                                                                                                                     CGGTGGTGGTGATGGACACGCAGGAGGCTGGGATCCGGCTCGTGCACGCGCTGCTGGCGT
                                                                                                                                                                                                            Plant Sciences Building,
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences have been trimmed below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Botany
The University of Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-Torgan: Anthraconse-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthraconse disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant, no effort was made to eliminate ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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197 c 1
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78.3%;
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Pred. No. 2.9e-33;
0; Mismatches 101;
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Best Local
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                                                                                                                                                                                    ctgtcgtcttgggtcgagagcatgctgtcggagctcaacgcgccgccgccgccgccctcccg
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                                                                                                                   gccgatcccctccccggccggcgacggccggccgacctgtccgccgactccgtgcg 545
                                                    -gcggctacttcgatctccgccctccgtcgactcctcc-agcagcatctacgcgctgcg
                                                                                                  CCAGCGCCGCCGCCCATGCTTCCACCTCGTCCACTGTCACCGGCGGCGGTGGT
                                                                                                                                                                   CTCTCCTCCTGGGTCGAGAGCATGCTTTCCGAGCTCAACGCGCCGCTGCCCCCTATCCCG
                                                                                                                                                                                                                                   GCGGATGACGGGTTCGTGTCGCACCTGGCCACGGACACCGTGCACTACAACCCCTCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki,T. and Yamamoto,K.
Rice cDNA from immature leaf including apical meristem Unpublished (1997)
On May 20, 1999 this sequence version replaced g1:48808 Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa.
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AU065169 Rice cDNA from
Oryza sativa cDNA clone
AU065169 CT COLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice Genome Research Program,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence updated (03-Feb-2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute of Agrobiological Resources
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tsasaki@abr.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 meristem
a 206 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="immature"
/note="Organ: leaf; immature leaf including
meristem (under long day condition)"
meristem (under long day condition)"
206 c 211 g 102 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meristem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Nipponbare"
/db_xref="taxon:4530"
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/clone_lib="Rice cDNA from immature leaf including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .596
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77.5%;
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Immature leaf including apical meristem E60220_2A, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URL:http://rgp.dna.affrc.go.jp/
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                                                                                                                                                                                                                                                                               Email: estewatson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
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                                                             /tissue_type="Hypocotyl and Plumule,
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                                            /note="Vector:
:: pT7T3Pac (Pharmacia); Site_1: EcoRI; This cDNA library was constructed from mRNA hypocotyl and plumule tissues of seeds
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RESULT 2
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; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Peng, Jinrong
; APPLICANT: Carol, Pierre
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APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI
FILE REFERENCE: 620-45
CURRENT APPLICATION NUMBER: US/09/117,853
CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: PCT/GB97/00390
EARLIER FILING DATE: 1997-02-12
EARLIER FILING DATE: 1997-02-12
EARLIER APPLICATION NUMBER: GB 9602796.6
EARLIER APPLICATION NUMBER: GB 9602796.6
EARLIER FILING DATE: 196-02-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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Pred. No. 3.8e-50;
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CURRENT APPLICATION NUMBER: US/09/117,853
CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: PCT/GB97/00390
EARLIER FILING DATE: 1997-02-12
EARLIER APPLICATION NUMBER: GB 9602796.6
EARLIER FILING DATE: 1996-02-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Best Local S
Matches 686
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APPLICANT: Harberd, Nicholas P
APPLICANT: Peng, Jinrong
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI
FILE REFERENCE: 620-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application Patent No. 6307126
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RESULT 4
US-09-17-853-5
; Sequence 5, Application US/09117853
; Patent No. 6307126
; GENERAL INFORMATION:

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APPLICANT: Carol, Pierre
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI ge:
FILE REFERENCE: 620-45
CURRENT APPLICATION NUMBER: US/09/117,853
CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: CT/GB97/00390
EARLIER FILING DATE: 1997-02-12
EARLIER APPLICATION NUMBER: GB 9602796.6
EARLIER FILING DATE: 1996-02-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
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APPLICANT: Harberd, Nicholas P
APPLICANT: Peng, Jinrong
APPLICANT: Peng, Jinrong
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI
FILE REFERENCE: 620-45
CURRENT APPLICATION NUMBER: US/09/117,853
CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: PCT/GB97/00390
EARLIER FILING DATE: 1997-02-12
EARLIER APPLICATION NUMBER: GB 9602796.6
EARLIER FILING DATE: 1996-02-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                             ; LENGTH: 1636
; TYPE: DNA
; ORGANIZM: Arabidopsis thallana
US-09-117-853-7
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Matches 695;
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Pred. No. 1.8e-46;
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agggttatcgggtggaggagtgacggctgtctcatgttggg 1636
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; LOCATION:
US-08-804-227C-7
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 641; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                   23076
                                                                                                 23019
                                                                                                                                                                 22959
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ZIP: 46285
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION (UMBER: 35,784
REFERENCE/DOCKET NUMBER: x-8231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES.
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                NAME/KEY:
LOCATION:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: LILLY CORPORTY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: THOMAS G. PLANT 1501 STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
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                                                                                                                                                             CGGTGACGACGCCCGGAGACCCGGCTCGGCTACCACGTCGCGTGGAAGGGACT 23018
gggcagcggcggctacttcgatctccgccctccgtcgactcctccagcagcatctacgc 479
                                   GGACCAGTACACCGCCCTCGCCGACACCCTGGAACAGGCGGTCGCCTCCTTCGGCGGAAC 23135
                                                     gccgccgcccctcccgcccgccgcagctcaacgcctccacctcctccaccgtcac 419
                                                                                               GCGCTCCA---CCACCGGCGGCTGGCGCCCCGGCCTGCTGATCGTGCCCACCGG 23075
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31329..36071
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350..14002
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                                                                                                                                                                                                                            Score 99.2; DB 2;
Pred. No. 1.4e-08;
0; Mismatches 748;
                                                                                                                                                                                                                                                          Length 44377;
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Query Match
Best Local Similarity
Matches 641; Conserv

Conservative

4.78;

Score 99.2; DB 2; Pred. No. 1.4e-08; 0; Mismatches 748,

Length 44377; Indels

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US-08-804-198-1
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                                                                                                                                                                                                                                                                                                                       TELEPHONE: 317-276-38 INFORMATION FOR SEQ ID NO:
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                                           NAME/KEY:
LOCATION:
FEATURE:
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NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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ADDRESSEE: PAUL R. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Richardson, Mark A.
APPLICANT: ROSteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
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                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/804,198 FILING DATE: CLASSIFICATION: 435
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CITY: INDIANAPOLIS
STATE: IN
                                                                                                      LOCATION:
                                                                                                                    NAME/KEY:
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                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                             TYPE: nucleic
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                                                                                                                                                                                                         NAME/KEY:
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LILLY CORPORATE CENTER
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317-276-3885
TD NO: 1:
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Richardson, Mark A.
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Microsoft Word 5.1
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
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APPLICANT: FLEISCHMAN, Robert
APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 692; Conserv
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                                         3929347 ATCCCGCGCCGCCGTCGCCGTCCCCACCGTCAC-CGCCTTGGCCGCCGGCGCGC
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totacgogotgoggateccctccccggccggcgacggcggccggccgacctgtccg
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Pred. No. 3.1e-08;
0; Mismatches 889;
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SOFTWARE: FastSEQ for Windows Version 3.0

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; LENGTH: 1931

; TYPE: DA

ORGANISM: EBNA

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APPLICANT: HOrlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903USI
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.3%; Score 91.8; DB 2; Best Local Similarity 45.9%; Pred. No. 1.9e-07; Matches 351; Conservative 0; Mismatches 412;
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GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin a
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
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Best Local Similarity 43.2%;
Matches 580; Conservative
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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TYPE: DNA
ORGANISM: Streptomyces venezuelae
-09-105-537-1
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Pred. No. 5.7e-07;
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US-09-105-537-32

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APPLICANT: Sherman, D.H.
APPLICANT: L1u, H.
APPLICANT: L1u, H.
APPLICANT: ZNac, Y.
APPLICANT: ZNac, L.
TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 11220
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; ORGANISM: Streptomyces
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Best Local Similarity 42.7%;
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Pred. No. 1.2e-06;
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RESULT 12
US-09-105-537-5
; Sequence 5, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26

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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
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Best Local Similarity
Matches 680; Conserv
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ORGANISM: Streptomyces
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Pred. No. 1.3e-06;
0; Mismatches 898;
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APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: 1906.72002120

CURRENT FILING DATE: 1999.05-27

EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-320-878-19; Sequence 19, Application US/09320878A; Patent No. 6117659.
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; EARLIER APPLICATION NUMBER: 60/087,080; EARLIER FILING DATE: 1998-05-28; NUMBER OF SEQ ID NOS: 34; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 19; LENGTH: 38506; TYPE: DATE ORGANISM: Streptomyces venezuelae US-09-320-878-19
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Best Local Similarity 44.4%;
Matches 641; Conservative
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Pred. No. 3.1e-06;
0; Mismatches 767;
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APPLICANT: Cheung,
APPLICANT: Wesley,
              APPLICATION NUMBER: US/07/
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis p
REGISTRATION NUMBER: 27976
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                                                                                                                                     CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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15 No. 5352596th University
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Ronald D.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 8438 base pairs

TELEFAX: TELEPHONE:

309-685-4128

309-685-4011 ext.513

HYPOTHETICAL: N MOLECULE TYPE:

NO

DNA (genomic) double

STRANDEDNESS: TOPOLOGY: lin TYPE: NUCLEIC ACID

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Best Local Similarity 46.3%;
Matches 349; Conservative (
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CCCGAGCAGCCCGGCCTCGTCGTCCCAGCGCCGGCGGCGGCGGCGGCGGCGCCCCTCC 4270
                 tcgtctctcggtgggggcgccaggagctctgtggtggaggctgccccgccggtcgcggcc 663
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Pred. No. 3.1e-06;
0; Mismatches 399;
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US-08-125-468-1
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GENERAL INFORMATION:
                                             Query Match
Best Local Similarity
Matches 616; Conserv
                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TSevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31.
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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151 gcggcgctcgggtacaaggtgcgcgcctccgacatggcggacgtggcgcagaagctggag 210
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 22-SEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 07470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
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Perfect score:
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## paclobutrazol. Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; Protein encoded by wheat Rht clone 5al genomic sequence. 16-JUL-1999 (first entry)

07-AUG-1998; WO9909174-A1: Triticum aestivum. 13-AUG-1997; 25-FEB-1999 98WO-GB02383

Result No.

Score

Match

Length

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Description

Protein encoded by Protein encoded by Zea mays protein f Human ATFx leucine

SUMMARIES

AAY02540 AAY02538

Query

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AAB80892 AAW21733 AAB95859

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Human protein sequ Protein encoded by Protein encoded by

AAB80893 AAG27119

AAB80896 AAB95274

AAY02543

Harberd NP,

Peng J, Richards

DE;

(PLAN-) PLANT BIOSCIENCE LTD.

97GB-0017192

WPI; 1999-181040/15. N-PSDB; AAX36279.

New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype

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RESULT AAYO2538
ID AAYO
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
                                                                                                                                                                                                                                                         antagonised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weedwarf but let crop plants grow tall. The present sequence is encoded the wheat Rht clone 5al genomic sequence.
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                                                                                                                                                                                                                                                         New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLAN-) PLANT BIOSCIENCE LTD.
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                                                                                                                                                                                                     English.
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RESULT AAG277119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by rice expressed sequence tag (EST) AAD39460, which is homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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99US-0130510.
99US-0130891.
99US-0131449.
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99US-0132484.
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99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
99US-0132863
99US-0134216
99US-0134218
99US-0134219
99US-0134221
99US-0134376
99US-0134768
99US-0134764
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99US-0130077.
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PR 21 - MAY 1999 99US-0135124 PR 24 - MAY 1999 99US-0135629 PR 27 - MAY 1999 99US-0135629 PR 27 - MAY 1999 99US-0135722 PR 27 - MAY 1999 99US-0135640 PR 16 - JUN 1999 99US-0133453 PR 16 - JUN 1999 99US-0133453 PR 18 - JUN 1999 99US-0133461 PR 18 - JUN 1999 99US-0133461 PR 18 - JUN 1999 99US-0133463 PR 18 - JUN 1999 99US-0143353 PR 22 - JUN 1999 99US-0143353 PR 23 - JUN 1999 99US-0143353 PR 24 - JUN 1999 99US-0143353 PR 25 - JUN 1999 99US-0143353 PR 26 - JUN 1999 99US-0143624 PR 16 - JUL 1999 99US-0143624 PR 17 - JUL 1999 99US-0143624 PR 18 - JUL 1999 99US-0143624 PR 19 - JUL 1999 99US-0143635 PR 19 - JUL 1999 99US-0143624 PR 19
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                               The present invention relates to a method for identifying a modulator of gamma aminobutyric acid_B (GABA_B) receptor-mediated activity, by monitoring the interaction between a CREB/ATF transcription factor capable of binding to GABA_B receptor. The present sequence is the leucine zipper domain of human ATFx (see AAB80892), which was used in the method of the present invention. ATFx is a member of the CREB/ATF family of transcription factors. ATFx contains a bZIP domain by which it interacts with the coiled coil domain of GABA_B receptor. Modulators of GABA_B receptor activity are useful for treating central nervous system
                                                                                                                                                                                                                                                                                          Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor and the CREB/ATF transcription factors in the presence of a test
                                                                                                Sequence
                                                                                                                      or peripheral nervous system disorders.
                                                                                                                                                                                                                                                          Claim 14; Page 64-65;
                                                                                                                                                                                                                                                                                                                                                                              White J,
                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-1999;
12-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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DB; AAF77878.
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99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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                                                75.0%;
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90.0%;
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                                                           DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor and the CREB/ATF transcription factors in the presence of a test
                                                         01-OCT-1997
                                                                                               AAW21733;
                                                                                                                              AAW21733 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White J, Wise A, Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-1999; 99GB-0020569.
12-JAN-2000; 2000GB-0000516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ATFx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ATFx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB80892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB80892 standard; protein; 216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                             pppplppap 73
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DB; AAF77877.
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                                                                                                                                                                                                                                                                                                         Similarity 100.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        216
                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                     75.0%; Scc
100.0%; Pr
                                                                                                                                    223 AA
                                                                                                                                                                                                                                                                                                                             Score 57; pred. No.
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                                                                                                                                                                                                                                                                                                         red. No. 13;
Mismatches
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                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                            Length 216;
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                                                                                                                                                                                                                                                                                                           Gaps
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밁 Q

NIP-1 encoded

by clone

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ARBSULT
AAB9589
ID AAB9
XX AAB9
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XX Huma
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XX EP10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               using the fusion proteins given in AAW21731-32. Compounds which interfere with the interaction of NuMA with a known NIP (NuMA interacting protein) are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP which may be markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein. This protein is rich in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAW21733-35 represent NuMA binding proteins (NuMA nuclear mitotic apparatus). These protein sequences were identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding nuclear mitotic appts. interacting proteins - useful for modulating cell division and proliferation
                                                                                                                      Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 28; Page 57-58; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McPherson SMG, Snyder MP;
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                                         07-FEB-2001
                                                                  EP1074617-A2
                                                                                                                                                 Human protein
                                                                                                                                                                          26-JUN-2001 (first entry)
                                                                                                                                                                                                       AAB95859;
                                                                                                                                                                                                                                 AAB95859 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      proline residues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malignant cell
            28-JUL-2000; 2000EP-0116126
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DB; AAT77784.
                                                                                                                                                                                                                                                                                                 pppplppap 10
                                                                                                                                                                                                                                                                                                                                                                                                                           223 AA;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NuMA; nuclear mitotic apparatus; NuMA interacting protein; proliferation; antibody; Ab; detection; l growth.
                                                                                                                                                 sequence SEQ
                                                                                                                    detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US09504.
                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                     75.0%;
                                                                                                                                                                                                                                                                                                                                                        Score 57; DB Pred. No. 13; 0; Mismatches
                                                                                                                                                 ID NO:18922
                                                                                                                                                                                                                                 282
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13;
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Human ATFx with N-terminal extension

Human; ATFx; gamma aminobutyric acid B receptor; GABA B receptor;

factor

08-MAR-2001

Homo sapiens

WO200116596-A2

30-MAY-2001

(first entry)

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Best Local
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH1874 represent human cDNA sequences; AAB92446 to AAH3639 represent human amino acid sequences; and AAH3629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 18922;
                                                                                                                                                                                                   AAB80896;
                                                                                                                                                                                                                              AAB80896 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugiyama
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                        75.0%;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                     DB
16;
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(, Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 282;
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Query Match
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Ota T, :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for identifying a modulator of gamma aminobutyric acid_B (GABA_B) receptor-mediated activity, by monitoring the interaction between a CREB/AFF transcription factor capable of binding to GABA_B receptor. The present sequence is human AFFx, which was used in the method of the present invention. AFFx is a member of the CREB/AFF family of transcription factors. AFFx contains a bZIP domain, by which it interacts with the coiled coil domain of GABA_B receptor. Modulators of GABA_B receptor activity are useful for treating central nervous system or peripheral nervous system disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor and the CREB/ATF transcription factors in the presence of a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-1999; 99GB-0020569.
12-JAN-2000; 2000GB-0000516.
                                                                                                                                                                   11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                               07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White J,
                                                                                 (HELI-) HELIX RES INST
                                                                                                                                                                                                                        29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                          28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence has an N-terminal extension compared to AAB80892.
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Isogai T, Nishikawa T,
, Sugiyama T, Wakamats
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                                                                                                                                    2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                          2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                           99JP-0300253.
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Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO:17476
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Pred. No.
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Hayashi K, S
A, Nagai K,
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16;
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Saito K, Y
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                            Yamamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                Harberd NP,
                                                                                                                                    07-AUG-1998;
                                                                                                                                                                                                                                                                                           paclobutrazol; maize.
                                                                                                                                                                                                                                                                                                           Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                               antagonist;
                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by the partial sequence of the maize D8-2023 allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY02543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY02543 standard; Protein; 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID 17476; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
                                                      (PLAN-) PLANT BIOSCIENCE LTD
                                                                                              13-AUG-1997;
                                                                                                                                                                          25-FEB-1999
                                                                                                                                                                                                                 WO9909174-A1
                                                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                              16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 lptpppppppppp 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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              Peng
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                              97GB-0017192.
                                                                                                                                    98WO-GB02383
                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%;
76.9%;
                Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
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RRESULT 1
AAVO2514
ID AAVOX
XX AAVOX
AC AAVC
XX AAVC
XX Rht
KW Rht
KW Ante
KW Pacl
XX YOU
DE Prot
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KW Ante
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as pacibutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the partial sequence of the maize D8-2023 allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes polypeptides encoded by the Rht gene (the its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09909174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; maize.
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                                                                                New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by maize lal genomic clone sequence.
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                           Disclosure; Fig
                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                            (PLAN-)
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82 lnappaplppa 92
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                                                                                                                                                                                                                                         1999-181040/15
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                                                                                                                                                                                                             AAX36280.
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                                                                                                                                                                                                                                                                                                Peng J,
                                                                                                                                                                                                                                                                                                                                                                                                                       97GB-0017192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-GB02383.
                               96;
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                           88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.7%;
                                                                                                                                                                                                                                                                                                    Richards DE;
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Pred. No.
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10;
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RESULT 1
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
                                                                                                                                                                                                                                                    12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                         vasotropic, antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; altergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer associated protein sequence SEQ ID NO:1119
                                                                                         Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing {\it e.g.} cancer -
                                                                                                                                          N-PSDB; AAC77883
                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000WO-US05882
                                                                                                                                                                                                                                                                                                                   21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                 WO200055350-A1
                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                              neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
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                                                                                                                                                                                       CA,
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                              drug screening.
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Pred.
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42;
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0;

AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities

Claim 11;

Page 1730-1731; 2352pp; English.

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ARESULT 1
AAB79117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corynebacterium gracumacum, organic acid; proteinogenic amino acid; fine chemical production; organic acid; proteinogenic amino acid; nucleoside; nucleoside; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering;
                                                                                                                                                                                                                                                                 09-JUL-1999;
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09-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               include: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                 14-JUL-1999
                                                                                                                                            14-JUL-1999;
14-JUL-1999;
                                                                                                                                                                                                    14-JUL-1999
                                                                                                                                                                                                                                        09-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brevibacterium; environmental condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum HA protein sequence SEQ ID NO:190
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Corynebacterium glutamicum

HA protein sequence SEQ ID NO:440

30-APR-2001 AAB79242;

(first entry)

fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme diagnosis; Corynebacterium diphtheriae; genetic engineering;

enzyme;

Corynebacterium glutamicum; homeostasis; adaptation; HA

protein

Brevibacterium;

environmental

condition

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288

297

1 LNAPPPPLPP 10 ldapppplpp

Matches

Conservative

Mismatches

0;

0;

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AAB79242

AAB79242 standard; Protein; 313

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CC AAF7113B to AAF71357 encode the Corynebacterium glutamicum homeostasis CC and adaptation (HA) proteins given in AAB79023 to AAB79242. The CC clls and production of fine chemicals, such as, an organic acid, proteins given in chemicals, such as, an organic acid, carbinoduction of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or CC proteinogenic or nonproteinogenic amino acid (preferred), purine or CC proteinogenic or nonproteinogenic amino acid (preferred), purine or CC proteinogenic or nucleoside, nucleotide, lipid, saturated or unsaturated or carbinogenic acid, proteinogenic or unsaturated or proteinogenic or proteinogenic or saturated or unsaturated or unsaturated or unsaturated or unsaturated or glutamate, aspartate, glycine, serine, threonine, glutamine, corporate, arginine, protline, histidine, corporate, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence or tryptophan. The fine chemical production can be modulated. The presence or activity of corynebacterium or corporate amino or can be used to map the C. glutamicum genome or can be used for diagnosing the proteins encoded by the (I) are used to maintain compositasis in C. glutamicum or help the microorganism to adapt to corporate or conditions.
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31-AUG-1999;
31-AUG-1999;
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CC AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis CC and adaptation (HA) proteins given in AAB79023 to AAB79242. The CC .glutamicum HA genes (I) can be used in vectors for expression in host C cells and production of fine chemicals, such as, an organic acid, C proteinogenic or nonproteinogenic amino acid (preferred), purine or C pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated CC fatty acid, diol, carbohydrate, aronatic compound, vitamin, cofactor, CC polyketide or enzyme. The amino acids produced can be lysine, glutamine, CC cysteine, valine, leucine, isoleucine, arginine, proline, methionine, CC glutamate, alanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are CC used for diagnosing the presence or activity of Corynebacterium. The HA proteins encoded by the C glutamicum genome or can be CC used as markers for genetically engineered Corynebacterium or Brevibacterium. The HA proteins encoded by the (I) are used to maintain CC homeostasis in C. glutamicum or help the microorganism to adapt to
  Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins or enzymes -
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14-JUL-1999;
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                                                                                               environmental conditions.
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 72.4%; ilarity 90.0%; Conservative
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A70856
A70857
T19721
T32889
I38707
T13478
S27200
S27200
S25292
A96529
                                                                                                                                                            I84718
C96734
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                                                       proline-rich prote
hypothetical prote
61K protein - Auto
unknown protein F2
                            hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
MHC class III hist
                                                                                                                            hypothetical prote
hypothetical prote
nuclear receptor c
HD protein - mouse
PHLP5A protein - c
                                                                                                                                                                                         hypothetical prote
cyclin-dependent k
H-2 region II bind
              high molecular mas
G2R protein - vari
                                                                                        hypothetical prote
Fas ligand - human
hypothetical prote
                                                                                                                                                                                                                           Description
                                                                                                                                                                   RXR-betal isoform
                                                                                                                                                                           retinoid X recepto
retinoic acid rece
      hypothetical prote
                                                                                                             probable lppz prot
hypothetical prote
                                                                                                                                                                                                                pherophorin-S - Vo
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Apporteit cal protein C26F1.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999
C; Accession: T15645
A; Description: The Sequence of C. elegans cosmid C26F1.
A; Reference number: Z18381
A; Reference number: Z18381
A; Accession: T15645
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-267 <GEI>A; Cross : references: EMBL:U53148; NID:g1255375; PID:g1255384; PIDN:AAB37073.1; GSPD
A; Experimental source: strain Bristol N2; clone C26F1
C; Genetics:
A; Gene : CESP:C26F1.1
A; Map position: 5
A; Introns: 54/3; 69/2; 85/2; 156/2: 171/3; 192/3

GSPDB:G

Query Match

72.4%; Score 55;

DB 2;

Length 267;

RESULT T15645

N

Ωy В

|||| ||||:| 216 NAPPSPLPPSP 226

NAPPPPLPPAP 12

A; Accession: A; Status: pre A; Status: pre A; Molecule ty; A; Residues: 1 A; Cross-refer; A; Experimenta. A; Note: in col C; Keywords: e: Query Match Best Local: Matches	RESULT T10798 pherophor C; Species C; Date: 1 C; Accessi R; Godl, K EMBO J. I A; Title: 1	C C C C C C C C C C C C C C C C C C C
A; Accession: T10/98 A; Actatus: preliminary; A; Molecule type: mRNA A; Residues: 1-599 <god> A; Cross-references: EMB A; Experimental source: A; Note: in contrast to C; Keywords: extracellul Query Match Best Local Similarity Matches 9; Conser</god>	RESULT 1 T10798 pherophorin-S - Volvox carteri C;Species: Volvox carteri C;Date: 16-Unl-1999 #sequence_ C;Accession: T10798 R;Godl, K; Hallmann, A.; Wenz EMBO J. 16, 25-34, 1997 A;Title: Differential targetti A;Reference number: Z17154; MU	52 68.4 52 68.4 52 68.4 52 68.4 52 68.4 52 68.4 52 68.7 51 67.1 51 67.1 51 67.1 51 67.1
A; Accession: TIU/98 A; Actatus: preliminary; translated A; Molecule type: mRNA A; Residues: 1-599 <god> A; Cross-references: EMBL:Y07752; A; Cross-imental source: strain HK A; Note: in contrast to the other C; Keywords: extracellular matrix; Ouery Match Best Local Similarity 81.8%; Matches 9; Conservative</god>	ox carteri rteri #sequence_1 , A.; Wenz! 997 217154; MU!	4 1460 1 4 1730 1 4 1872 2 4 1896 2 4 11896 2 4 11958 2 4 12123 2 4 2123 2 4 2123 2 4 2123 2 4 2123 2 1 294 2 1 399 2 1 399 2 1 541 2 1 564 2 1 566 2
A; Accession: TIU/96 A; Actatus: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-599 <god> A; Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032. A; Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032. A; Experimental source: Strain HK 10; sub_species Nagariensis: A; Note: in contrast to the other pherophorins, pherophorin-S C; Keywords: extracellular matrix; glycoprotein; pheromone C; Keywords: extracellular matrix; glycoprotein; pheromone Ouery Match Best Local Similarity 81.88; Pred: No. 16; Best Local Similarity 81.88; Pred: No. 16; Matches 9; Conservative 1; Mismatches 1; Indels</god>	ALIGNMENTS  RESULT 1  T10798  pherophorin-S - Volvox carteri C;Species: Volvox carteri C;Date: 16Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul C;Accession: T10798 R;Godl, K; Hallmann, A; Wenzl, S.; Sumper, M. EMBO J. 16, 25-34, 1997 A;Title: Differential targetting of closely related ECM-glycoproteins: A;Reference number: Z17154; MUID:97162277	EDBEIF B45344 T124683 B72175 B72175 B72175 B40505 B40505 F86348 F86348 F769150 A759150 A759150 A759150 A759150 A759166 A759160 A7591666
d from GB/EMBL/DDBJ  NID:g1655698; PIDN:CAA69032 10; sub_species Nagariensis: pherophorins, pherophorin-s; glycoprotein; pheromone  Score 56; DB 2; Length 5: pred. No. 16; pred. No. 16; pred. No. 16; pred. No. 16;		
CAA69032.1; ariensis: phorin-S is omone Length 599; ; Indels	text_change	immec hypot probb hypot D15R hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot hypot h
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 20-Sep-1999
C;Accession: A34418
R;Hamada, K; Gleason, S.L.; Levi, B.Z.; Hirschfeld, S.; Appella, E.; Ozato, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 8289-8293, 1989
A;Title: H-ZRIIBP, a member of the nuclear hormone receptor superfamily that binds to bd A;Reference number: A34418; MUID:90046782
                                                       C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: D41727
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R;Tang, D.; Yeung, J.; Lee, K.; Matsushita, M.; Matsu J. Biol. Chem. 270, 26897-26903, 1995
A;Title: An isoform of the neuronal cyclin-dependent A;Reference number: I39172; MUID:96070784
A;Accession: I39172
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 A;Title:
                   R;Leid, M.; Kastner, P
Cell 68, 377-395, 1992
                                                                                                                retinoid X receptor beta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-446 <HAM>
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A; Residues: 1-367 < RES>
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Best Local Similarity
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9; Conser
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9; Conser
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                                     P.; Lyons,
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72.7%;
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and
                                     R.; Nakshatri,
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                                                                                                                                                                                                                                                                                                       Score 55; DB
Pred. No. 16;
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); Mismatches
RXR identity of the
                                                                                                                                                                                                                                                                                         Mismatches
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                                     H.; Saunders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN: AAC50278.1;
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HeLa
cell factor with which RAR
                                     M.; Zacharewski,
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                                   T.;
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         A;Gene: Rxrb
A;Introns: 76/1; 148/3; 201/1; 261/1; 362/1; 406/2; 437/1; 472/2
C;Superfamily: retinoic acid receptor alpha; erbA transforming protein homology
F;190-436/Domain: erbA transforming protein homology <ERBA>
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                                                                                                              A; Cross-references:
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C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 20-Aug-1999
C;Accession: 184718
R;Nagata, T.; Kanno, Y.; Ozato, K.; Taketo, M.
Gene 142, 183-189, 1994
A;Title: The mouse Rxrb gene encoding RXR beta: genomic organization and two A;Reference number: 148752; MUID:94252565
A;Accession: 184718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A41651
R;Yu, V.C.; Delsert, C.; Andersen, B.; Holloway, J.M.; Devary, O.V.; Naeaer, A.M.; Ki
Cell 67, 1251-1266, 1991
A;Title: RXRbeta: a coregulator that enhances binding of retinoic acid, thyroid hormo
A;Reference number: A41651; MUID:92103690
A;Accession: A41651
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retinoic acid receptor coregulator - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M81766; NID:g206602; PIDN:AAA42025.1; PID:g206603 (;Superfamily: unassigned erbA-related proteins; erbA transforming prote C;KeyWords: zinc finger C;KeyWords: zinc finger F;121-367/Domain: erbA transforming protein homology <ERBA>
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                      A; Molecule type: DNA
A; Residues: 1-520 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-451 < YUA>
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A; Accession: D41727
                                                                                                                                                                                                                                                                     RXR-betal isoform -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source:
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Best Local S
Matches 8
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Best Local
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                                                                preliminary; translated from GB/EMBL/DDBJ
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8; Conser
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8; Conservative
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GB:D21831; NID:g497828; PIDN:BAA04858.1;
                                                                                                                                                                                                                                                                     mouse
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55;
Pred. No.
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    PID:g987669
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1 LNAPPPP----LPPAP 12
                Conservative
                        71.1%;
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                        Score 54;
Pred. No.
                Mismatches
                        DB
45;
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                1;
                               Length 998;
                Indels
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               Gaps
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F15H11.18 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                     A; Map position: I
A; Introns: 54/3;
A; Note: D1007.7
                                                                                                                                                                                 A;Cross-references: EMBL:AF003151; PIDN:AAB54225.1
A;Experimental source: strain Bristol N2; clone D1
                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, August 1999
A;Description: The sequence of C. elegans cosmid D1007
A;Reference number: Z20934
A;Accession: T30930
                                                                                                                                                                                                                                                                                                                                                                   R; Davidson, S.;
                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein D1007.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-138 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A86141;
A; Accession: C96734
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                                                                                                                                                                                                                           A; Residues: 1-998 < DAV>
                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                                                      314/2; 532/1;
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72.78;
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Pred. No. 6.4;
1; Mismatches
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Pred. No.
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                                                                                                                      711/3; 756/3; 907/2; 939/1
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                                                                                                                                                                               clone D1007
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PHIP5A protein - common timothy (fragment)
C;Species: Phleum pratense (common timothy)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Mar-1995
C;Accession: S32101
R;Bufe, A.; Becker, W.M.; Petersen, A.; Schramm, G.; Schlaak, M.
submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1521,2002-3119 <RE2>
A;Cross-references: GB:LJ3313; NID:g438806; PIDN:AAA37800.1; PID:g438807
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HD protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I49729; I49730
R;Lin, B.; Nasir, J.; MacDonald, H.; Hutchinson, G.; Graham, R.; Rommens, J.M.; Hay
Hum. Mol. Genet. 3, 85-92, 1994
A;Title: Sequence of the murine huntington disease gene: evidence for conservation
A;Reference number: I49729; MUID:94214482
A;Accession: I49729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 08-Oct-1999
C;Accession: S60254
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                            submitted to the EMBL Data Library, February 1993
A;Description: Phl pV (timothy grass) major allergen bears at least two B-cell epitop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L23312; NID:g438804; PIDN:AAA37799.1; PID:g438805
A;Accession: I49730
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A; Reference number: A; Accession: S32101
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A; Residues: 1-3119 < RES>
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9; Conserv
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8; Conserv
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81.8%;
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Pred. No. 1.4e
0; Mismatches
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Pred. No.
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1.1e+02;
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A;Map position: X
A;Introns: 54/3; 149/3; 183/1; 224/2; 273/2; 330/3; 378/3; 416/1;
C;Superfamily: Caenorhabditis elegans hypothetical protein C34E11.
                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-731 <WIL>
                                                                                                                                                                                                                                                                                                R;McMurray, A.
submitted to the EMBL Data Library, November 1995
s;Reference number: Z19169
A;Accession: T19721
A;Accession: T19721
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A;Molecule type: mRNA
A;Residues: 1-257 <BUF>
A;Cross-references: EMBL:X70942
C;Superfamily: grass pollen allergen
                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C34E11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL021287; GB:AL123456; NID:g3261508; PIDN:CAA16091.1; PID:e12377
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987
A;Accession: A70856
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A70856
                                                                                                                                                                                                              A;Cross-references: EMBL:267754; PIDN:CAA91752.1; GSPDB:GN00028; CESP:C34E11.2
A;Experimental source: clone C34E11
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A; Residues: 1-373 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rjandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: A70856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable lppZ protein - Mycobacterium tuberculosis (strain H37RV)
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R:Graves, T.; Sutterer, C.; Hawkins, M.; Wilson, R. submitted to the EMBL Data Library, January 1998
A;Description: The sequence of C. elegans cosmid C34B2.
A;Reference number: Z21241
A;Accession: T32889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C34B2.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
Search completed: January 22, 2002, 16:24:48 Job time: 68 sec
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A; Introns: 35/3; 91/2; 200/2
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A;Residues: 1-238 <GRA>
A;Cross-references: EMBL:AF043693; PIDN:AAB97541.1; GSPDB:GN00019; CESP:C34B2.9
A;Experimental source: strain Bristol N2; clone C34B2
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ATF5_H
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=20558615; PubMed=11087824;

White J.H., McIllhinney R.A.J., Wise A., Ciruela F., Chan W.Y.,

White J.H., McIllhinney R.A.J., Wise A., Ciruela F., Chan W.Y.,

Emson P.C., Billinton A., Marshall F.H.;

"The GABAB receptor interacts directly with the related transcription factors CREB2 and ATTX.";

Factors CREB2 and ATTX.";
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09Y2D1; 09UN03;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-5 (ACT TRANSCRIPTION FACTOR ATFX).

ATF5 OR ATFX.
         EMBL; AF305687; AAG22558.1; -.
EMBL; AB021663; BAA78477.2; -.
EMBL; AF101388; AAD28370.1; -.
InterPro; IPR002637; Hamlp_like.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR001871; bZIP.
                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                  "Pati D., Meistrich M.L., Plon S.E.;
"Human Cdc34 and Rad6B ubiquitin-conjugating enzymes target repressors of cyclic AMP-induced transcription for proteolysis.";
Mol. Cell. Biol. 19:5001-5013(1999).
-i- FUNCTION: THIS PROTEIN BIDDS THE CAMP RESPONSE ELEMENT (CRE)
-(CONSENSUS: $'GTGACGT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN MANY
VIRAL AND CELLULAR PROMOTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 161-282 FROM N.A. MEDLINE=99303793; PubMed=10373550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kohroki J., Tanaka K. Submitted (DEC-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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RESULT 2
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DOMAIN 186 194
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CONFLICT 161 163
SEQUENCE 282 AA; 30674 M
                                                                            Hypothetical
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15-JUL-1998 (Rel. 36, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN KIAA0298 (FRAGMENT).
                                                                                                                                                                                                                                                                 Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which ca code for large proteins in vitro."; DNA Res. 4:141-150/1997\
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                     EMBL; AB002296; BAA20758.2; -.
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
Nagase T., Ishikawa K.-I
Miyajima N., Kotani H.,
Submitted (DEC-1999) to
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PROSITE; PS00036;
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Mammalia; Eutheria;
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                                                                                                                          PS50119; ZF_BBOX;
                                                                                                                                                                                                                                                                                                                                                                                          Ishikawa K.-I., Seki N., Nakajima D., Ohira J., Kotani H., Nomura N., Ohara O.; (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                     901 AA;
                                                                             93
                                                                                                               protein;
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    DNA-binding; Activator;
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DDB2F907CA0215A0.CRC64;
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_MOUSE
__MOUSE STANDARD; PRT; 369 AA.

CDS__MOUSE STANDARD; PRT; 369 AA.

O35926; O35277;

15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 5 ACTIVATOR 2 PRECURSOR (CDK5 ACTIVATOR CYCLIN-DEPENDENT KINASE 5 REGULATORY SUBUNIT 2) (P39) (P391).
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SEQUENCE
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Q13319;
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CHAIN
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J. Biol. Chem. 270:26897-26903(1995).
-I- FUNCTION: ACTIVATOR OF CDK5/TPKII.
-I- SUBUNIT: HETERODIMER OF A CATALYTIC SUBUNIT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 5 ACTIVATOR 2 PRECURSOR (CDK5 ACTIVATOR 2)
(CYCLIN-DEPENDENT KINASE 5 REGULATORY SUBUNIT 2) (P39) (P391).
CDK5R2 OR NCK5AI.
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MEDLINE-96070784; PubMed-7592934;
Tang D., Yeung J., Lee K.-Y., Mat
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-!- TISSUE SPECIFICITY: BRAIN AND NEURON SPECIFIC.
-!- SIMILARITY: BELONGS TO THE CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hatase O., Wang J.H.;
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CYCLIN-DEPENDENT KII
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01-OCT-1996 (Rel. 3
20-AUG-2001 (Rel. 4
RETINOIC ACID RECEI
                   RETINOIC A (FRAGMENT)
                                                                                                                      RXRB_RAT P49743;
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"Comparative analysis of gene expression of the cyclin-dependent Kinase 5 (cdk5) activators p35 and p39 in the rat CNS and embryonic development revealed distinctive overlap with cdk5.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTIVATOR OF CDK5/TPKII.
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"Molecular cloning and characterisation of a mouse gene encoding an isoform of the neuronal cyclin-dependent kinase 5 (CDK5) activator.";
Biochim. Biophys. Acta 1398:371-376(1998).
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Mus musculus (Mouse).
Chordata;
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OR NR2B2 OR RCOR-1
                                                                                                                                                                                                                                                   PPPPPPPAPQ 164
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                                                                                                                                                                                                                                                                                                                                 Similarity
9; Conserv
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75 78
1.55 163
48 351
17 91
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38914 MW;
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                                        RECEPTOR
                                                                                                                                              STANDARD;
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                                                          . 34, Created)
. 34, Last sequ.
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Last annotation updat
                                    RXR-BETA (NUCLEAR RECEPTOR CO-REGULATOR
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POLY-SER.

G -> V (IN
S -> G (IN
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S -> R (II)
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S -> R (II)
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                                                                                                                                                                                                                                                                                                                                                                     Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
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Best Local (
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                                                PXRB_MOUSE STANDARD;
P28704; P33243;
O1-DEC-1992 (Rel. 24, Creat,
O1-FEB-1996 (Rel. 33, Last;
20-AUG-2001 (Rel. 40, Last;
RETINDIC ACID RECEPTOR RXR-1
BINDING PROTEIN H-2RIIBP)
                                                                                                                                         MOUSE
FI
                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                            DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
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Yu V.C., Delsert (
 Eukaryota; Metazoa;
Mammalia; Eutheria;
                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00104; hormone_rec;
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yu V.C., Delsert C., Andersen B., Holloway J.M., Devary O.V.,
Naeaer A.M., Kim S.Y., Boutin J.M., Glass C.K., Roesenfeld M.G.;
"RXR beta: a coregulator that enhances binding of retinoic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                        RXRB OR NR2B2
                                                                                                                                                                                                                                                                                                                                                                                                           Zinc-
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M81766; HSSP; P19793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
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                                                                                                                                                                                                                2 NAPPPPLPPAP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: NUCLE DOMAIN: CONTOCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: INVOLVED IN 9-CIS RETINOIC ACID (9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NR2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                           SAPPPPMPPPP
                                                                                                                                                                                                                                           Similarity
8; Conserv
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130
130
166
196
256
458
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                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                                                129
195
150
190
255
Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                        49078
                                                                                                                                                                                                                                                      72.4%;
                                                               Last annot
R RXR-BETA
                                                                                                      Created)
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                                                                             annotation
                                                                                       sequence
                                                                                                                                                                                                                                         Score 55; DB Pred. No. 13; 2; Mismatches
                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                          NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                        LIGAND-BINDING (BY 22D11956B11DB4BE
                                                                                                                                                                                                                                                                                                                                HINGE
                                                                                                                                                                                                                                                                                                                                                                                  MODULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
 Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                (MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACID
                                                                                       update)
                                                                n update)
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13;
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                                                                                                                              A
                                                               I REGULATORY ELEMENT
                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                   Length 458
                                                                                                                                                                                                                                                                                                        SIMILARITY) CRC64;
  Euteleostomi; 
murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-TERMINAL DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY
                                                                                                                                                                                                                                            0;
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EMBL;
EMBL;
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"The mouse Rxrb gene encoding RXR beta: genomic mRNA isoforms generated by alternative splicing initiated from CpG island promoters.";
                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oro A.E., Kakizuka A., Evans R.M.; ""Characterization of three RXR genes that mediate the rethnoic acid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92192447; PubMed-1312497;
Mangelsdorf D.J., Borgmeyer U., He
Oro A.E., Kakizuka A., Evans R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90046782; PubMed-2554307; Hamada K., Gleason S.L., Levi B.-Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            efficiently."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Purification, cloning, and RXR which RAR or TR heterodimerizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chambon P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leid M., Kastner P., Lyons R., Nakshatri H., Saunders M. Zacharewsi T., Chen J.Y., Staub A., Garnier J.M., Mader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92127595; PubMed-1310259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 73-520 FROM N.A. (LONG
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 75-520 FROM N.A. (LONG ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 68:377-395(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
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                  MGD; MGI:98215;
                                                BL; D21831; BAA04858.1; JBL; D21830; BAA04859.1; JBL; D21830; BAA04859.1; JBL; D21830; BAA04859.1; JBL; D21830; BAA04859.1; JBL; M26804; AAA40081.2; BL; M26804; AAA37772.1; BL; M26024; CAA46963.1; BL; M26024; CAA46963.1; A34418; A34418.
                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR:
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM (SHOWN ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: IN ALL TISSUES TESTED INCLUDING BRAIN, THYMUS SPLEEN AND LIVER.
SPLEEN AND LIVER.
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: INVOLVED IN RETINOIC ACID RESPONSE PATHWAY. BINDS 9-CIS RETINOIC ACID (9C-RA). BINDS TO BOTH, CLASS I REGULATORY ELEMENT OF MAJOR HISTOCOMPATIBILITY CLASS I GENES (CRE) AND THE ESTROGEN RESPONSE ELEMENT (ERE).
                                                                                                                                                                                                                                                                                                                                                             NR2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IIBP, a member of the nuclear hormone receptor superfamily that to both the regulatory element of major histocompatibility I genes and the estrogen response element."; Natl. Acad. Sci. U.S.A. 86:8289-8293(1989).
IPR000536; Hormone_rec_lig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6:329-344(1992)
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                                                                                                                       JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identity of the HeLa cell factor with to bind target sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heyman R.A., Zhou J.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOFORM)
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RESULT 7
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MNT_MOUSE

J 008789; p97349;

T 15-DEC-1998 (Rel. 37, Created)

T 15-DEC-1998 (Rel. 37, Last sequence update)

JT 15-DEC-1998 (Rel. 37, Last annotation update)

T 15-DEC-1998 (Rel. 37, Last annotation update)

MYC AN
A Meroni G., Reymond A., Alcalay M., Borsani G., Tanigami A.,
Tonlorenzi R., Lo Nigro C., Messali S., Zollo M., Ledbetter D.
A Brent R., Ballabio A., Carrozzo R.;
"Rox, a novel billible protein expressed in quiescent cells tha
heterodimerizes with Max, binds a non-canonical E box and acts
heterodimerizes with Max, binds a non-canonical E box and acts
ranscriptional repressor.";
EMBO J. 16:2892-2906(1997).
-i- FUNCTION. BINDS DAA AS A HETERODIMER WITH MAX AND REPRESSE
TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE 5'-CA
AND, WITH HIGHER AFFINITY, TO 5'-CACGCG-3'.
AND, WITH HIGHER AFFINITY, TO 5'-CACGCG-3'.
BINDS DAA AS AN HOMODIMER OR A HETERODIMER W
-i- SUBCLLULAR LOCATION: NUCLEAR.
-i- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00104; hormone_rec; 1. Pfam; PF00105; zf-C4; 1. PF100105; STRODETINGER. PRINTS; PR00047; STROHORMONER. PRINTS; PR00398; STROHORMONER. PRINTS; PR00545; RETINOIDXR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                  Hurlin P.J., Queva C., Eisenman R.N.;
"Mnt, a novel Max-interacting protein is coe
proliferating cells and mediates repression
Genes Dev. 11:44-58(1997).
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription_regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001723;
InterPro; IPR001628;
                                                                                                                                                                                             TISSUE-Embryo;
MEDLINE-97327566; PubMed-9184233;
                                                                                                                                                                                                                                                                                                                      TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       MEDLINE=97152466; PubMed=9000049;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NAPPPPLPPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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192
228
258
318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene family; Alternative splicing.

1 191 MODULATING (BY SIMILARITY).
     BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                            Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strdhormone_rcptor
zf-C4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE.
HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGAND-BINDING (BY SIMILARITY).
MISSING (IN SHORT ISOFORM).
SGR -> MGP (IN REF. 2).
RDS -> EFP (IN REF. 3).
L -> M (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71FAEAECOD2DB505 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              (MYC AN
                                                                                                                                                                                                                                                                              coexpressed with Myc
                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTAGONIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                             DIMERIZATION WITH ANOTHER OR A HETERODIMER WITH MAX
                                                                                                                                                                                                                                                                  at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 520
                                                                                                                                                                   Tanigami A.,
M., Ledbetter D.H.,
                                                                                                                                                                                                                                                                  Мус
                                                                                                                                                                                                                                                                  binding
                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                            Murinae;
                                                                     REPRESSES
NCE 5'-CACGTG-3'
                                                                                                                            acts
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RESULT
NCR1_H
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001092; HLH_dim. Pf4am; PF00010; HLH; 1. SMART; SM00353; HLH; 1. PRORTIES MO0353; HLH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U77356; AAB38687.1; -. EMBL; Y07609; CAA68878.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
"Prediction of the coding sequences of unidentified human genes, XIV The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                         Kikuno R., Nagase T., Ishikawa K.-I., Hiro
Tanaka A., Kotani H., Nomura N., Ohara O.;
                                                                                                                                         transcription
complex.":
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                 NCOR1 OR KIAA1047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:109150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                      Kikuno R.,
                                                                     MEDLINE-99397452;
                                                                                  TISSUE-Brain;
                                                                                             SEQUENCE OF 782-2440 FROM N.A.
                                                                                                                                                                 "ETO, fusion
                                                                                                                                                                                         MEDLINE=98393736; PubMed=9724795;
                                                                                                                                                                                                       TISSUE=Fetal brain;
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PPPPLPPAPQ 13
                                                                                                                                                                            J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPPLPPAAQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iption
                                                                                                                                               Hoshino T., Redner R.L., Kajigaya S., Liu J.M.; sion partner in t(8;21) acute myeloid leukemia, repreption by interaction with the human N-CoR/mSin3/HDAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00038;
                                                      Nagase
                                                                                                                       Acad. Sci. U.S.A. 95:10860-10865(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
272
301
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414
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528
63311)
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                                                                     PubMed=10470851;
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90.0%;
                                                    Ishikawa K.-I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEUCINE-ZIPPER (POTENTIAL).

T -> P (IN REF. 2).

V -> A (IN REF. 2).

EE -> QO (IN REF. 2).

G -> A (IN REF. 2).

V -> A (IN REF. 2).

A -> P (IN REF. 2).

A -> P (IN REF. 2).

A -> A (IN REF. 2).

A -> A (IN REF. 2).
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ressor; Nuclear protein; DNA-binding.
BASIC MOTIF (POTENTIAL).
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3F4E61A10CF4142F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                      Hirosawa M., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions ng as its content is in
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 6:197-205(1999).
[3]
[3]
SEQUENCE OF 974-2440 FROM N.A.
MEDLINE=99375328; PubMed=10444336;
                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                 DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB0195
MIM; 600849;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF044209; AAC33550.1;
EMBL; AB028970; BA882999.1;
EMBL; AB019524; BA875814.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagaya T., Chen K.-S., Fujieda M., Horwitz K.B., Lupski J.R., Seo H.; "Localization of the human nuclear
        SEQUENCE
                                                                                                                                                                                                                                                                                              Nuclear protein; Transcription regulation; DNA-binding; Repressor; Coiled coil.
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00249; myb_DNA-binding; SMART; SM00395; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>-</del>
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                                                                                                                                                                                                                                                      DOMAIN
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                                                                               NIAMOC
                                                                                              DOMAIN
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                           PROSITE; PS50090;
                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001005; Myb_DNA_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2 AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTORAND REPRESENTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B) SIMILARITY: CONTAINS 2 CORNR BOX.
SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAINS (ID1 AND ID2).

DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED DOMAIN: THE TWO INTERACTION DOMAINS. THIS MOTIF IS REQUIRED SEQUENCE REFERENCE TO AS THE CORNR BOX. THIS MOTIF IS REQUIRED SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUIREMENTS THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B AND HISTONE DEACETYLASES HDAC1 AND HDAC2. THIS COMPLEX ASSOCIATES WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THABSENCE OF LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.
                                                                                                                                    174
254
299
437
625
501
507
988
2055
2263
        A,
                                                                                                                                    216
312
328
482
670
557
617
1816
2059
2267
                                                                                                                                                                                                                                                                                                                              MYB.
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1963
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L -> v (+:
PP -> SS
W -> R (I
Q -> H (I
Q -> H (J
                                                                                                                                   CORNE BOX OF CORNE BOX OF POLY-GLN.
                                                                                                        POLY-ALA.
POLY-PRO.
                                                                                                                                                                                                                          COILED COIL (POTENTIAL)
SANT-A (POTENTIAL).
SANT-B (POTENTIAL).
                                                                POLY-SER.
L -> V (IN REF.
                                                                                                                                                                                                           COILED COIL (POTENTIAL)
                                                                                              POLY-ALA.
                                                                                                                                                                                                                                                                COILED COIL (POTENTIAL).
INTERACTION WITH SIN3A/B
                                                                                                                                                                                INTERACTION WITH ETO
       > SS (IN REF. 2).
> R (IN REF. 2).
> H (IN REF. 2).
50A4D7964D00EDAB CRC64;
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                                        2).
2).
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Best Local
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                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCR1_MOUSE STANDARD; PRT; 2453 AA. Q60974; Q60812; Q60974; Q60812; Q70-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) NUCLEAR RECEPTOR CO-REPRESSOR 1 (N-COR1) (N-COR) (RETINOID X RECEPTOR
                  modified and this entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seol W., Choi H.S., Moore D.D.;
"Isolation of proteins that interact
receptor: two novel orphan receptors.
Mol. Endocrinol. 9:72-85(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1792-2453 FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Ligand-independent repression mediated by a nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoerlein A.J., Naeaer A.M., Heinzel T.,
Kurokawa R., Ryan A., Kamei Y., Soedersi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Pituitary;
MEDLINE-96008539; PubMed-7566114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95280959; PubMed=7760852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCOR1 OR RXRIP13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTING PROTEIN 13) (RIP13).
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                                                                                                                                                                 SIMILARITY: (
SIMILARITY: (
SIMILARITY: I
                                                                                                                                                                                                                                      DOMAINS (ID1 AND ID2).

DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED SEQUENCE REFERRED TO AS THE CORNR BOX. THIS MOTIF IS REQUIRED AND SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                          ABSENCE OF LIGAND.

SUBCELLULAR LOCATION: NUCLEAR.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: UBIQUITOUS.

TISSUE SPECIFICITY: UBIQUITOUS.

TOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2 AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-
INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SINJA/B AND HISTONE DEACETYLASES HDAC1 AND HDAC2. THIS COMPLEX ASSOCIATES WITH THE THEROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPPPLPPPPE 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377:397-404(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                 CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B) CONTAINS 2 CORNR BOX.
BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.1%;
is not removed. Usage 23 is not removed. Usage 23 is not removed. Usage 23 is not removed.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  co-repressor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thyroid hormone
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troem M., Glass
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lass C.K.,
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; Murinae; Mus
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statement a license

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HD_MOUSE
ID MANA
AC P428
AC P428
AC P428
AC P428
AC O1-0
DT 01-0
DT 01-0
DE HUNT
GN HD G
OS Mus
OC Euka
OC MANA
OC NCBII
RN [1]
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RN [1]
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RN [2]
RY MEDI
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RA Romm
RT repe
RL Hum.
RN [2]
RP SEQU
RC STT;
RA Barr
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Best Local
                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=94278649; PubMed=8009370;

Barnes G.T., Duyao M.P., Ambrose C.M., McNeil S.,

Srinidhi J., Gusella J.F., Macdonald M.E.;

"Mouse Huntington's disease gene homolog (Hdh).";

"Mouse Huntington's disease gene homolog (Hdh).";
                                                                                                                                                                                                                                                                                                                 HD_MOUSE
P42859;
01-NOV-1995
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
SEQUENCE
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DNA_BIND
DOMAIN
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DOMAIN
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                                                                                                                                      conservation, alternate splicing
repeat.":
                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN HOMOLOG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50090; MYB_3; 1.
Nuclear protein; Transcription regulation;
Coiled coil; Alternative splicing.
                                                                                                                                                                                           STRAIN=C57BL/6; TISSUE=Brain, and MEDLINE=94214482; PubMed=8162057;
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00249; myb_DNA-binding; SMART; SM00395; SANT; 2.
 MEDLINE=95375771;
           SEQUENCE FROM
                                                                                                                                    repeat.
                                                                                                                                                           Rommens J.M., Hayden M.R.;
"Sequence of the murine Huntington disease gene: evidence for
                                                                                                                                                                                   Lin B.,
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                              HD OR HDH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001005;
                                                                                                                                                                                                                                                                                                                                                                                                                              606
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8; Conserv
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                                                                                                                     Genet. 3:85-92(1994)
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2277
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616
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 PubMed=7647777
                                                                                                                                                                                Macdonald H., Hutchinson
                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.18;
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Pred. No.
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CORNR BOX OF CORNR BOX OF
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POLY-ALA.
POLY-SER.
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POLY-ALA.
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SANT-B (POTENTIAL).
COILED COIL (POTENTIAL).
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INTERACTION WITH SIN3A/B
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN
                                                                                                                                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> T (IN REF. 2).
-> P (IN REF. 2).
; 52208B40382F7E6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                              and
                                                                                                                                                                                                        Spleen;
                                                                                                                                                                                                                                                                                                                                                                   3119
                                                                                                                                              polymorphism
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82;
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ID2.
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                                                                                                                                                                                G., Graham R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOFORM)
                                                                                                                                               'n
                                                                         Persichetti
                                                                                                                                                                                                                                                                                                        (HD PROTEIN).
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                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                               a
                                                                                                                                                                                                                                                         Murinae;
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                                                                                                                                              triplet
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EMBL; L23312; AAA37799.1; -.
EMBL; L23313; AAA37800.1; -.
EMBL; L28827; AAA89100.1; ALT_SEQ.
EMBL; L28423; AAC52218.1; -.
EMBL; L34024; AAA91085.1; -.
EMBL; L34024; AAA91085.1; JOINED.
EMBL; L34021; AAA91085.1; JOINED.
EMBL; L34022; AAA91085.1; JOINED.
EMBL; L34023; AAA91085.1; JOINED.
    DOMAIN
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CONFLICT
CONF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I- SUBCELLULAR LOCATION: CYTOPLASMIC.
-I- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING SEEMS TO GIVE RISE TO A 480 AMINO ACIDS SHORTER ISOFORM. THIS PRODUCT CANNOT BE EXPLAINED BY A SIMPLE SPLICING EVENT.
-I- TISSUE SPECIFICITY: THE HIGHEST LEVEL IS SEEN THROUGHOUT THE BRAIN, BUT IT IS ALSO FOUND IN THE STOMACH, HEART, TESTIS, ADIPOSE TISSUE, MUSCLE, SPLEEN, LIVER, AND KIDNEY.
-I- DEVELOPMENTAL STAGE: PREDOMINANT EXPRESSION IN NEURONAL TISSUES AT ALL DEVELOPMENTAL STAGES, IN 14.5 DAY OLD EMBRYOS, IT IS ALSO DETECTED IN NON-NEURONAL TISSUES. THIS EXPRESSION IS DOWN-REGULATED IN LATER STAGES OF DEVELOPMENT.
-I- POLYMORPHISM: THE FIRST POLY-PRO REPEAT STRETCH DIFFERS IN LENGTH BY ONE UNIT (THREE) IN MUS SPRETUS STRAIN CONFARED TO OTHER STRAINS, (FOUR), THE POLY-GLN REGION DOES NOT APPEAR TO BE POLYMORPHIC, EXPLAINING THE ABSENCE OF A MURINE HD-LIKE DISORDER.
-I- SIMILARITY: BELONGS TO THE HUNGTINTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Genomics 25:707-715(1995).
-I- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trottier Y., Devys D., Imbert G., Saudou F., An I., Lutz Y., Weber C., Agid Y., Hirsch E.C., Mandel J.L., "Callular localization of the Huntington's disease protein and discrimination of the normal and mutated form."; Nat. Genet. 10:104-110(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of the 5' region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldberg Y.P., Hayden M.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VESICLE FUNCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000091; Huntingtin.
                                                                                                                                                                                                                                                                                                                                                         1512
                                                                                                                                                                                                                1417
1696
2615
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POLY-GLU.
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                                                G (IN REF. C)                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat.
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20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYCLIN T1 (CYCLIN T) (CYCT1).
SEQUENCE FROM N.A., AND MUTAGENES TISSUE-Fibroblast; MEDLINE-99145542; PubMed-9990016; Fujinaga K., Taube R., Wimmer J.,
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99059742; PubMed=9843510;
Bieniasz P.D., Grdina T.A., Bogerd H.P., Cullen B.R.;
"Recruitment of a protein complex containing Tat and
governs the species specificity of HIV-1 Tat.";
EMBO J. 17:7056-7065(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                   and a critical cysteine residue
CycTl protein.";
                                                                                                                                                                                                                                                                                  MEDLINE=99051315; PubMed=9832504; Garber M.E., Wei P., KewalRamani V.N., Mayall T.P., Herrmann C.H., Rice A.P., Littman D.R., Jones K.A.; "The interaction between HIV-1 Tat and human cyclin T1 requires zinc
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                                                                                         Tat-activation.";
J. Mol. Biol. 288:57-69(1999).
                                                                                                                          Kwak Y.T., Ivanov D., Guo J., Nee E., Gaynor R.B.;
"Role of the human and murine cyclin T proteins in
                                                                                                                                                             MEDLINE=99263519; PubMed=10329126;
                                                                                                                                                                                TISSUE=Spleen;
                                                                                                                                                                                                                                    Genes
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Mammalia; Eutheria;
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   Taube R., Wimmer J., Cujec T.P., Peterlin B.M.;
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                                                       MUTAGENESIS
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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060563; 060581;
20-AUG-2001 (Rel. 4
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20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
CYCLIN T1 (CYCLIN T
CCNT1.
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Proc. Natl. Acad. Sci. U.S.A. 96:1285-1290(1999).

-i- FUNCTION: REGULATORY SUBUNIT OF THE CYCLIN-DEPENDENT KINASE PAIR (CDK9/CYCLIN T) COMPLEX, ALSO CALLED POSITIVE TRANSCRIPTION ELLONGATION FACTOR B (P-TEFB), WHICH IS PROPOSED TO FACTILITATE THE TRANSITION FROM ABORTIVE TO PRODUCTION ELONGATION BY PHOSPHORYLATING THE CTD (CARBOXY-TERMINAL DOMAIN) OF THE LARGE SUBUNIT OF RNA POLYMERASE II (RNAP II). DOES NOT BIND EFFICIENTLY TO THE TRANSACTIVATION DOMAIN OF THE HIV-1 NUCLEAR TRANSCRIPTIONAL
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SEQUENCE
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DOMAIN
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 SEQUENCE FROM N.A., ANI
TISSUE=T-cell lymphoma;
MEDLINE=98150851; PubMe
                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                     Homo sapiens (Human)
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InterPro; IPRO00553; Cyclin.
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SUBUNIT: ASSOCIATES WITH CDK9 TO FORM P-TEFB. CYCLIN T1 IS
PREDOMINANT CYCLIN ASSOCIATED WITH CDK9.
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONG TO CYCLIN SUBFAMILY.
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AF109179;
AF087662;
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AAD19654.1; -...
AAD17798.1; -...
AAD17798.1; -...
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40, Last sequence update)
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T) (CYCT1).
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   PubMed=9491887
                                                                          Chordata;
Primates;
                               AND PARTIAL SEQUENCE.
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COLLED COLL (POTENTIAL).
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V -> M (IN REF. 3).
V -> M (20 REF. 3).
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                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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J. VITOL. 73:5777-5786(1999).

LCOMPLEX, ALSO CALLED POSITIVE TRANSCRIPTION ELONGATION FACILITATE THE ELONGATION FACTOR B (P-TEFB), WHICH IS PROPOSED TO FACILITATE THE ELONGATION FACTOR B (P-TEFB), WHICH IS PROPOSED TO FACILITATE THE PHOSPHORYLATING THE CITD (CARBOXY TERMINAL DOMAIN) OF THE LARGE SUBUNIT OF RNA POLYMERASE II (RNAP II). BINDS ALSO TO THE TRANSACTIVATION DOMAIN OF THE HIV-1 NUCLEAR TRANSCRIPTIONAL ACTIVATOR, TAT. IT IS PROBABLY THE CIS-ACTING TRANSACTIVATION RESPONSE ELEMENT (TAR) RNA-BINDING COFACTOR FOR TAT. ALSO SERVES AS AN ESSENTIAL COFACTOR FOR HIV 2-TAT AND SIMIAN IMMUNODEFICIENCY VIRUS (AFRICAN MANDRILL) THAT FUNCTION.

-I- SUBUNIT: ASSOCIATES WITH CDK9 TO FORM P-TEFB. CYCLIN T1 IS THE PREDOMINANT CYCLIN ASSOCIATED WITH CDK9.

-I- SUBCELLULAR LOCATION: NUCLEAR.

-I- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.

-I- WISCELLANEOUS: INTERRACTION BETWEEN TAT AND CYCLIN T1 REQUIRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garber M.E., Wei P. Rice A.P., Littman "The interaction be
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MEDLINE=98167917; PubMed=9499409;
Peng J.-M., Zhu Y., Milton J.T., Price D.H.;
"Identification of multiple cyclin subunits of cenes Dev. 12:755-762(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tat and RNA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CycT1
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Gaynor R.B.;
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e interaction between HIV-1 Tat and human
a critical cysteine residue that is not o
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AF045161;
AF048730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92:451-462(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garber M.E., Fang S.-M., Fischer W.H., Jones K.A.; l CDK9-associated C-type cyclin interacts directly mediates its high-affinity, loop-specific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. 288:57-69(1999).
                                                                                                                          non-profit institu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12:3512-3527(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for tat-activation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288:41-56(1999).
  AAC39638.1;
AAC39664.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9832504;
                                                                                                                                                       institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KewalRamani V.N., Mayall
                                                                                                                             is not removed
                                                                                                                                                                                                          ght. It is produced through a collaboration
Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.,
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                                                                                                     (See http://www.isb-sib.
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conserved
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ins in
                                                                                                                          Usage by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulating HIV-1
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of Tat-cyclin
                                                                                                                                                                               restrictions
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                                                                                                                                                                                                                                                                                       SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAR RNA
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Q
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                                                                                                                                                                 RA Bieniasz P.D., Grdina T.A., Bogerd H.P., Cullen B.R.;

RT "Highly divergent lentuviral Tat proteins activate viral gene
RT expression by a common mechanism.";

RL Mol. Cell. Biol. 19:4592-4599(1999).

CC (CDK9/CYCLIN T) COMPLEX, ALSO HIGHED POSITIVE TRANSCRIPTION

CC (CDK9/CYCLIN T) COMPLEX, ALSO HIGHED POSITIVE TRANSCRIPTION

CC (CDK9/CYCLIN T) COMPLEX, ALSO HIGHED POSITIVE TO FACILITATE THE

CC (CDK9/CYCLIN T) COMPLEX, ALSO HIGHED POSITIVE TO FACILITATE THE

CC (CDK9/CYCLIN T) COMPLEX, ALSO HIGHED POSITIVE THE ARGE THANSITION FACM ABORTIVE TO PRODUCTION ELONGATION BY

PHOSPHORYLATING THE CTD (CARBOXY-TEMNIAL DOMAIN) OF THE LARGE

CC SUBUNIT OF RNA POLYMERASE II (RNAP II) (BY SIMILARITY). BINDS ALSO

CC TO THE TRANSACTIVATION DOMAIN OF THE EQUINE INFECTIOUS ANEMIA

CC VIRUS (ELAV) NUCLEAR TRANSCRIPTIONAL ACTIVATOR, TAT. IT IS

CC PROBABLY THE CIS-ACTING TRANSACTIVATION RESPONSE ELEMENT (TAR)

CC PROBABLY THE HIV-1 NUCLEAR TRANSCRIPTIONAL ACTIVATOR.

CC DOMAIN OF THE HIV-1 NUCLEAR TRANSCRIPTIONAL ACTIVATOR.

CC SUBUNIT: ASSOCIATES WITH CDK9 TO FORM P-TEFB. CYCLIN T1 IS THE

CC PREDOMINART CYCLIN ASSOCIATED WITH CDK9.

CC --- SUMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.

CC --- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
CCT1_HORSE
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Best Local
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20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
CYCLIN TI (CYCLIN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription redomain 253
DOMAIN 254
DOMAIN 384
DOMAIN 517
DOMAIN 560
DOMAIN 717
MUTAGEN 261
CONFLICT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCT1_HORSE
Q9XT26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
SEQUENCE
                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
             EMBL; AF137509; AAD38518.1; -.
                                              or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99303751; PubMed=10373508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000553; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 602506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00385; CYCLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00292; CYCLINS; FALSE_NEG.
IPR000553;
                                              email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         last;
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0 , 0 , 0
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526
570
725
261
77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80684 MW;
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80.0%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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POLY-PRO.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C->Y: LOSS OF HIV-1 TAT TRANSACTIVATION Q -> R (IN REF. 2).
4637EFB2DDEDFE13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL). POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). TAT: TAR RECOGNITION MOTIF (TRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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33;
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Best Local
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SEQUENCE
                                                               Wilkinson
Submitted
                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN
TNFSF6 OR APTILG1 OR FASL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
P48023;
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                                                                                                                                                                                                                        specificity
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                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription
                                                                                                                                                                            Submitted
                                                                                                                                                                                                                               Takahashi T., Tanaka M., Inazawa J., "Human Fas ligand: gene structure, c
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=95105731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00292;
                                  TISSUE=Blood;
                                             SEQUENCE OF 1-10 FROM
                                                                                SEQUENCE FROM N.A.
                                                                                                                                       Mita
                                                                                                                                                MEDLINE-95071350;
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                     Schaetzlein
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-95127560; PubMed-7826947;
                                                                                                                                                                                                                                                                                      lymphocytes."
                                                                                                                                                                                                                                                                                                        Alderson M.;
                                                                                           Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     718
                                                                                                                                                                                             EQUENCE FROM
                                                                                                                    Role of Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PPPPLPPAPQ 13
                                                                                                                                                                                                                                                                              Exp. Med. 181:71-77(1995).
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                                                                                                  Biophys.
                                                                                                                                      Hayashi N.,
                                                                                                                                                                                                                                                                                                                                                      ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           (JUN-1995)
                                                              (MAY-1997) to
                                                                                                                                                                                   C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         718
727 i
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519
562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulation; Nuclear protein 253 270
                                                                                                                                                                                                                                                                                                mediates activation-induced cell death
                                                                                                                             Kamada
                                                                                                                                                                                                              6:1567-1574(1994)
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995) to the
                                                                                                  Res.
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e; Cell division; Coiled coil;
                                                                                                                                  PubMed=7980502;
N., Iio S., Takehara T., Hijioka T., Kasahara
                                                                                                                                                                                                                                                                                                                   PubMed=7528780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427
528
573
                                                                                                                    in apoptosis induced by hepatitis
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80.0%;
                                             N.A.
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                                                               the
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                                                                                                                                                                           R., Philippsen P., Eibel H., EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53;
Pred. No.
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POLY-SER.
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COILED COIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAT: TAR RECOGNITION MOTIF (TRM) (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                  204:468-474(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                ., Abe T., Suda T., Nagata S.; chromosomal location and species
                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                           update)
LIGAND)
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33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           (APTL).
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JR FALLOW, JR. PROSITE; PMO0207; TNE; 1.

DR PROSITE; PS00251; TNE_1; 1.

DR PROSITE; PS00252; TNE_2; 1.

DR PROSITE; PS00249; TNE_2; 1.

ET PROSITE; PS00249; TNE_2; 1.

ET PROSITE; PS00249; TNE_2; 1.

ET DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).

ET TRANSHEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

ET DOMAIN 4 70 PRO-RICHLULAR (POTENTIAL).

ET DOMAIN 45 65 POLY-PRO.

ET DOMAIN 45 65 POLY-PRO.

ET CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).

ET CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).

ET CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 261 260 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 261 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
SMN_MOUSE
ID SNNL,M
AC P9780
DT 01-NO
DT 20-AU
DE SURVI
GN SMNL M
OC EUKAR
OC EUKAR
OC MARMAN
OC NCBI
RN [1]
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                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ro
NCBI_TaxID=10090;
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997801; 009092;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SEQUENCE FROM N.A.

MEDLINE-97224505; PubMed-9070939;

Viollet L., Bertrandy S., Brunialti A.L.B., Lefebv

Clermont O., Cruaud C., Guenet J.-L., Munnich A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 SURVIVAL MOTOR NEURON SMN1 OR SMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom;
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InterPro; IPR000478;
Pfam; PF00229; TNF;
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SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
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SUBCULIT: HOMOTRIMER (PROBABLE).

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X89102; CAA61474.1; -.
2, U08137; AAC50071.1; -.
2, U18127; AAC50124.1; -.
2, D38122; BAA07320.1; -.
2, D38122; BAA07320.1; -.
3, Z96050; CAB09424.1; -.
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P01375; 2T
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8; Conserv
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Rodentia;
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88.9%;
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TNF_family.
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Pred. No. 17;
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   Lefebvre S., Bu
ch A., Melki J.;
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Best Local S
Matches 8
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REPORT NATI ACAD. SCI. U.S.A. 94:9920-9925(1997).

REPORT NATIONAL THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPLICEOSOMAL SURVEY AND IS REQUIRED FOR PRE-MRNA CONTROL OF MOTOR SPLICING IN THE NUCLEUS (BY SIMILARITY).

REPORT NATIONAL STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR SPLICING PROTEIN INTERACTING PROTEIN 1 (SIP1/GEMIN2), GEMIN3 AND COMPLEX IS THOUGHT TO PLAY AN ESSENTIAL ROLE IN BIOGENESIS OF THE SMALL NUCLEAR RIBONUCLEOPROTEIN PARTICLES (SURNPS). INTERACTS WITH FIBRILLARIN AND WITH SEVERAL SPLICEOSOMAL SURNP CORE SM PROTEINS, INCLUDING B/B', SM D AND SM E PROTEINS (BY SIMILARITY).

RESURCELULAR INCCATION: CYTOPLAMIC AND NUCLEAR. LOCALIZED IN SUBGELLULAR INCCATION: CYTOPLAMIC AND NUCLEAR. LOCALIZED SM CONTROL OF ARE HIGHLY ENRICHED IN SPLICEOSOMAL SURNPS (BY SIMILARITY).
                                                                                                                                                           SMART; SM00333; TUDOR; 1.

mRNA processing; RNA-binding; N
DOMAIN 196 PC
DOMAIN 212 222 PC
DOMAIN 239 243 PC
SEQUENCE 288 AA; 31254 MW;
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                                                                                                                                                                                                                                                                                    EMBL; U63294; AAC53057.1;
EMBL; U77714; AAC53144.1;
EMBL; Y12835; CAA73356.1;
MGD; MGI:109257; Smn.
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MEDLINE-97264340; PubMed-9110173;
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Genomics 40:185-188(1997).
                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.1sb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse embryos."
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STRAIN-BALB/C; TISSUE-Brain;
MEDLLNE-97420785; PubMed-9275227;
Schrank B., Goetz R., Gunnersen J.M., Ure J.M., Toyka K.V.,
Schrank B., Goetz M.,
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"Inactivation of the survival motor neuron gene, a candidate gene for survival motor neuron gene, a candidate gene for survival motor neuron gene, a candidate gene for survival motor neuron gene.
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                                 PPPPLPPAP 12
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ron gene: homolog of the
                                                                      Conservative
222
                                                                                      68.4%;
88.9%;
                                                                                                                                                           ig; Nuclear protein.
polr-pro.
polr-pro.
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W; 757B3074649F7458 CRC64;
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Pred. No.
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Search completed: January Job time: 339 sec

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Q99mx7 mus musculu
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homo sap			oryza :	Q9deg1 gallus gall	Q9sbm1 volvox cart	Q9n5d3 caenorhabdi	=	~	Q9fip7 arabidopsis	Q9rcx9 streptomyce	Q9vuc6 drosophila	001864 caenorhabdi			Q9y103 drosophila	Q91k78 arabidopsis	Q9z0g8 rattus norv	Q62775 rattus norv	Q99j35 mus musculu	Q9vhtl drosophila	Q9vnd7 drosophila	Q9vmk3 drosophila	Q9ssk0 arabidopsis	Q9z118 rattus norv	Q9tv66 oryctolagus

## ALIGNMENTS

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01-MAY-2000
01-MAY-2000
01-JUN-2001
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
GIBBERELLIN RESPONSE MODULATOR.
Q9U1B2 PRELIMINARY;
Q9U1B2;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                           modulators.";
Nature 400:256-261(1999).
EMBL; AJVA2531; CAB51555.1; -.
SEQUENCE 623 AA; 65337 MW;
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MEDLINB=99347734; PubMed=10421366;

Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,

Plintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F.,

Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;

""Green revolution' genes encode mutant gibberellin response
                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum (Wheat).
Eukaryota; Virdiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. NIPPONBARE;
MEDLINE-20179680; PubMed-10713441;
Ogawa M., Kusano T., Katsumi M., Sano H.;
"Rice gibberellin-insensitive gene homolog, OsGAI, encodes a nuclear-
"Rice gibberellin-insensitive gene activation at transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A physical map of the Leishmania Genome Res. 8:135-145(1998).
EMBL; AL117324; CAB55537.1; -.
Hypothetical protein.
SEQUENCE 180 AA; 20276 MW; 1F7
  Q9BSA1
                                                                                                                                                                                                                                                                                                                                  Gene 245:21-29(2000)
EMBL; AB030956; BAA9
SEQUENCE 625 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).

Gryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ivens A.C., Lewis S.M., Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuchs M., Gabel C., Mueller-Auer S., Schaefer Ivens A.C., Lawson D., Quail M., Rajandream M. Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSGAI
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10; Conserv
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                                                                                                                                                                                                                  Conservative
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  PRELIMINARY;
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$65406 MW;
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pred. No.
1; Mismatc
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Last annotation update)
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  PRT;
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A., Barrell B.G.;
databases.
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Q9AA59;
01-JUN-2001
01-JUN-2001
01-JUN-2001
044708 PRELIMINARY;
044708; Q9VE64; Q9VE65;
01-JUN-1998 (TREMBLrel. 06,
01-JUN-2000 (TREMBLrel. 14,
                                                                                                                                                                                                                                                   Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., Potocka I., Nelson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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CC0747
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ACTIVATING TRANSCRIPTION FACTOR 5.
                                                                                                                                                                                                                   Complete proteome. SEQUENCE 407 AA;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=21173698;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Caulobacter crescentus.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC005174; AAH05174.1; -. SEQUENCE 282 AA; 30690 MW; B6D4CB6F631655B1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Caulobacter
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Pred. No.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Balcon R.C., Rogers Y.-H.C., Blaze's R.G., Champe M., Pfelifer B.D.,
RA Balcon R.C., Rogers Y.-H.C., Blaze's R.G., Champe M., Pfelifer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C.,
Durbin K.J., Bensen B.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dehlke C., Davenport L.B., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Dleet Z.S.M.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Diegwam C.,
RA Harris N.L., Keitham G.S., Pan S., Pollard J., Wei M.-H., Nelson D.L.,
RA Harls M., Wolfer C.D., Kraft C., Kravitz S., Kulp D. Lai Z.,
RA McInul W., Murphy B., Murphy L., Muzy D.M., Nelson D.L.,
RA Harls M., Weilsen K.A., Nixon K., Nusskern D.R., Smith T.,
RA Mount S.M., Woodage T., Worley R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Syler B., Shand M., Shang G., Zhao Q., Zhao Q., Zhao 
FlyBase; FBgn0004652; fru.
InterPro; IPR000210; BTB_POZ.
InterPro; IPR000561; EGF-like.
InterPro; IPR000822; Znf-C2H2.
Pfam; PF000651; BTB; 1.
Pfam; PF00096; zf-C2H2; 1.
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FRUITLESS PROTEIN, ISOFORMS MALE, FEMALE, 3 AND 4 (FRUITLESS CLASS I
MALE ISOFORM) (FRUITLESS CLASS I FEMALE ISOFORM) (CG7690 PROTEIN).
FRU OR CG7688 OR CG7689 OR CG7690.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                              -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 3 (SHOWN HERE AND 5 (AC P91618); ARE PRODUCED BY ALTERNATIVE EMBL; AF039231; AAB9677.1; --
EMBL; AE003722; AAF55564.1; --
EMBL; AE003722; AAF55565.1; ALT_TERM.
EMBL; U72492; AAB92662.1; --
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Cell 87:1079-1089(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97133215; PubMed=8978612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALE, FEMALE, 3 AND 4 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND FEMALE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽
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                                                                                                                                                                                                                                                                                                                                                                                                           3 (SHOWN HERE), 4, MALE, FEMALE Y ALTERNATIVE SPLICING.
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Query Match
Best Local Similarity
"-+-hes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                           fruitless expression.";
Nat. Cell Biol. 0:0-0(2000).
EMBL; AF220177; AAG28588.1; -.
FlyBase; FB9n0004652; fru.
InterPro; IPR000210; BTB_POZ.
InterPro; IPR000822; Znf-C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                              Q9GU21
Q9GU21;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alternative splicing; DNA-binding; EGF-like domain; Glycoprotein; Zinc-finger.

VARSPLIC 1 101 MISSING (IN FEMALE ISOFORM AND ISOFO
                                                                   DNA-binding; Me
                                                                                                                             pfam; pF00651; BTB; 1.
pfam; pF00096; zf-C2H2; 1.
sMART; SM00225; BTB; 1.
sMART; SM00355; ZnF_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                        FRUITLESS TYPE-A. FRU OR CG7688 OR CG7690.
                                                                                                                                                                                                                                                  Awano W., Nakata H., Piao Z.F., "Formation of the male-specific
                                                                                                                                                                                                                                                                            Usui-Aoki K., Ito H.,
                                                                                                                                                                                                                                                                                        STRAIN-CANTON
                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 VRAPPPPLPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LNAPPPPLPPAP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
9; Conser
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PS01186;
                                                                                         PS50097; BTB; 1.
PS00028; ZINC_FINGER_C2H2_1; 1.
PS50157; ZINC_FINGER_C2H2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      862 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324
                                                                    Metal-binding; Zinc-finger.
156 AA; 103051 MW; 675260937C937FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                        S;
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EGF_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92593
                                                                                                                                                                                                                                                   , Ui-Tei K., Takahashi K., Lukacsovich T.,
Piao Z.F., Nilsson E.E., Tomida J., Yamamoto D.;
le-specific muscle in female Drosophila by ectopic
                      75.0%;
75.0%;
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75.0%;
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17,
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                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; Pred. No.
                      Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAALKREYHPLHYMAANGGHNGPSALGYGNQGSGNAPNSAG
GAGSVAGGVGAGGAGGATGAAGHNSHHTMSYHNMFTPSRD
PGTMMRCRSCGKEYTNRWHHFHSHTAQRSMCPYCPATYSRI
DTLRSHLRVKHPDRLLKLNSSI (IN ISOFORM MALE
ISOFORM AND FEMALE ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQVQGAQHARHTMQSPAAHDVPLFAASSAPPIPHRLPRRGG
LLTARGQQSGLPGQQWSGAAVGFEHLPWPRKPPTPPASAIS
HTSQSLAEL -> SSARHHLSTPLSTSSSASPPPPPFGMHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVKCFNIKHDRHPDRELDRNHREHDDDPGVIEEVVVDHVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEAGNEHDPEEMKEAAYHATPPKGGLRIGIGYLCGWRLQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94C229E991526701 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               956
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1.9;
                                  DB 5;
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                                  Length 956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Conservative

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                    Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RRA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RGA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Ra Borkova D., Botchan M.R., Bouck J., Bokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Bartis N.I., Harrish M., Glasser K.,
Bartis N.I., Barten M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BQQ4;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Amid C., Hankeln T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VNZ6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465
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A., Gong F.,
N.L., Harvey
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9; Conser
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chromosome
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A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeed M.P., McPherson D.,

RA Liu X., Mattei B., McIntosh T.C., McCard M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nalson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;

RT The genome sequence of Drosophila melanogaster.";

EMBL; AE003595; AAF51766.1.

DR EMBL; AE003595; AAF51766.1.

B67F87AC2B2D3A45 CRC64;
                                                                                                                                                     Query Match
Best Local
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O'Callaghan D., Cazeviellle C., Allardet-Servent A., Bourg G.,
Foulongne V., Fruitos P., Kulakov Y., Ramuz M.;
"A homologue of the Agrobacterium tumefaciens VirB and Bordetella
pertussis Ptl Type IV secretion systems is essential for intracellular
surrival of Brucella suis.";
Mol. Microbiol 33:1210-1220(1999).
EMBL; AF141604; AAD56620.1; -
EMBL; AF141604; AAD56620.1; -
SEQUENCE 391 AA; 41453 MW; A6DCA4C9AFBB490D CRC64;
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O9RPX5;

O1-MAY-2000 (TrEMBLrel. 13,

O1-MAY-2000 (TrEMBLrel. 13,

O1-MAY-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBI_TaxID=29461;
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Q9ST48;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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Eukaryota; Viridiplantae;
Volvocaceae; Volvox.
NCBI_TaxID=3067;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GIBBERELLIN RESPONSE MODULATOR (FRAGMENT).
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01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                         Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M., Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F., Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P., "Green revolution' genes encode mutant gibberellin response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99347734; PubMed=10421366;
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Spermatophyta; Magnoliophyta;
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EMBO J. 16:25-34(1997).
EMBL; Y07752; CAA69032.1; -.
Mendel; 14875; Volca;2392;14875.
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                                                                                                                                                                                                                                                                                                           Nature 400:256-261(1999).
EMBL; AJ242530; CAB51557.1;
NON_TER 630 630
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                                                                                     LNAPPAPLPPA 120
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                                                                                                                                                                                                                                                                                      66028 MW;
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yta; Liliopsida; Poales; Poaceae; PACC clade;
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Pred. No.
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8BAA14D5A71F8082 CRC64;
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Q99pJ1;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
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InterPro; IPR001214; SET.
InterPro; IPR003166; POSTSET.
Pfam; PF00856; SET; 1.
PROSITE; PS50280; SET; 1.
SMART; SM00508; POSTSET; 1.
SMART; SM00317; SET; 1.
SMART; SM00317; SET; 1.
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Kikuno R., Nagase T., Ishikawa K., Hirosawa
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unide:
The complete sequences of 100 new cDNA clone:
for large proteins in vitro.";
DNA Res. 6:197-205(1999)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                       "The mouse ames waltzer hearing-loss podhi5, a novel protocadherin gene.", Nat. Genet. 27:99-102(2001).
EMBL; AF281899; AAG55891.1; -.
SEQUENCE 1943 AA; 214816 MW; E3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIAA1076
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MEDLINE-20578757; PubMed-11138007;
Alagramam K.N., Murcia C.L., Kwon
Woychik R.P.;
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RC STRAIN-BRISTOL N2;

RX MEDLINE-94150718; PubMed-7906398;

RX MEDLINE-94150718; PubMed-7906398;

RX MISSON R., Alascough R., Anderson K., Baynes C., Berks M.,

Wilson R., Alascough R., Connell M., Copsey T., Cooper J., Coulson A.,

RA Bonfield J., Burton J., Connell M., Favello A., Fulton L.,

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

RA Jones M., Kershaw J., Kirsten J., Laister N., Callaghan M.,

RA Jones M., Fersy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

Theory-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT "1.2 Mb of Contiguous nucleotide sequence from chromosome III of C.
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STRAIN-BRISTOL N2;
Geisel C., Stellyes L., Bradshaw H.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Similarity 90.0%;
9; Conservative
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## ALIGNMENTS

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New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibbereilin, used to confer a dwarf phenotype
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N-PSDB; AAX36279.
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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;

Protein encoded by wheat Rht clone 5al genomic sequence.

16-JUL-1999 (first entry)

AAY02540 standard; Protein;

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                                                                                ARSSVVEAAPPVAAAANATPALPVVVVDTQEAGIRLVHALLACAEAVQQENLSAAEALVK 258
 SVFEMHRLLAQPGALEKVLGTVRAVRPRIVTVVEQEANHNSGTFLDRFTESLHYYSTMFD
                                        DETDALQQVGWKLAQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGEEDPNEEPEVIAVN
                           detdalqqvgwklaqfahtirvdfqyrglvaatladlepfmlqpegeedpneepeviavn
                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pmologue; Triticum aestivum; wheat; growth inhibition;
gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peng J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-0017192.
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                                                                                                                                                                                                                                                                  68.2%;
100.0%;
                                                                                                                                                                                                                                                                  Score 425; pred. No.
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RESULT AAYOZ541
ID AAYO
AX Rht
KW Rht
KW Anta
KW Prot
XX PRO
PR 13-J
PR 13-J
PA (PLJ
XX N-P;
PT Anta
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                                                                                  The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by glbberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds the material and compared by the plant of the plants grow tall. The present sequence is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by maize lal genomic clone sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 9b; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harberd NP, Peng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PLAN-) PLANT BIOSCIENCE LTD
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLEGGSSGGGPSEVSSGAAAAPAAAGTDQVMSEVYLGRQICNVVACEGAERTERHETLGQ
                                                        lal genomic clone sequence.
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Query Match Best Local Similarity

21.2%; 100.0%;

Score 132; Pred. No.

DB 20; 3.9e-105;

Length

Matches

Conservative

0;

Mismatches

Query Match Best Local Similarity

11.4%;
100.0%;

Score 71; pred. No.

DB 20; 1

Length 138; Indels

0;

Gaps

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RESULT
AAY02544
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                     its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the partial sequence of the wheat rht-10 allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY02544 standard;
                                                                                                                                                                                                                                                             New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum.
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                                                                                                                                                                                                                                    Disclosure; Fig 12b; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by the partial sequence of the wheat rht-10 allele
Sequence
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                                                                                                                                                                                            specification describes polypeptides encoded by the Rht gene (
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                                                                                                                                                    Query Match
Best Local :
                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                   plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by rice expressed sequence tag (EST) AAD39460, which is homologous to the
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                                                                                                                                                                                                    wheat Rht gene.
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      227
                           221 PVVVVDTQEAGIRLVHALLACAEAVQQEN 249
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                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                         256 AA
                                                                                                                  4.7%;
llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6b; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97GB-0017192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γď
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richards DE;
                                                                                                                     0
                                                                                                                                                 Score 29; DB 20;
Pred. No. 7.9e-17;
                                                                                                                     Mismatches
                                                                                                                                                                         Length 256;
                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
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RESULT
AAW30794
ID AAW3
XX
AC AAW3
AC AAW3
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AC 19-W
XX
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                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the partial sequence of the maize D8-2023 allele.
                                                                                              AAW30794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                      AAW30794 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes polypeptides encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 11d; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX36282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY02543 standard; Protein; 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harberd NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY02543;
                                                                                                                                                                                                                                                                                                                                         51 SDMADVAQKLEQLEMAMGMGGVG 73
                                                                                                                                                                                                                                                                                                         35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                         sdmadvaqkleqlemamgmggvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999-181040/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 100 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omologue; Triticum aestivum; wheat; growth inhibition;
gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; pred. No.
                                                                                                                                                      259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 123;
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19-MAR-1998

(first entry)

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AAW38194
ID AAW3
XX
AC AAW3
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DT 11-N
XX
DE Arak
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Best Local Similarity
"~+~hes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the Arabidopsis thaliana gibberellin in sensitivity (gai-d2) gene product (GAI-d2), the expression of which inhibits plant growth. However the inhibition is antagonised by gibberellin (GA), while gai expression confers a dwarf phenotype that is insensitive to GA. Manipulating gai-d2 and GAI-d2 expression can produce tall or dwarf plants, particularly the latter for increased resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the regettive state until treated with GA, useful to inhibit bolting in spinach and lettuce. GAI-d2 can be used to raise specific antibodies for identifying homologous proteins or genes in other species. gai-d2 fragments can also be used as probes or primers to identify and clone related sequences, or in the preparation of antisense or sense expression regulating (co-suppressing) sequences. Rice plants that express GAI-d2 may be resistant to Bakane disease. Manipulation of gai-d2 and GAI-d2 makes it possible to tailor the degree of dwarfism and GA sensitivity to particular crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dwarf phenotype; lodging resistance; increased yield; flowering regulation; bolting inhibition; spinach; lettuce antibody; identification; probe; primer; antisense; sense; expression regulation; co-suppression; rice; Bakane disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carol P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Fig 6d; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding gibberellin inhibitor GAI and related antisense sequences - used to create tall, or particularly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9729123-A2.
                 Arabidopsis SCARECROW SRPa2 protein.
                                               11-MAY-1998 (first entry)
                                                                                      AAW38194;
                                                                                                                   AAW38194 standard; Protein; 262 AA
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants, especially crops such as maize, rice and wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INNE-) INNES CENT INNOVATIONS LTD JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gibberellin insensitivity; gai-d2; plant growth inhibition,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana gibberellin insensitivty gai-d2 gene product.
                                                                                                                                                                                                      229
                                                                                                                                                                                                                                      314 CPYLKFAHFTANQAILEAF 332
                                                                                                                                                     œ
                                                                                                                                                                                                   cpylkfahftangaileaf 247
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                                                                                                                                                                                                                                                                                                                                                          259 AA;
                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                     3.0%; Score 19;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peng J,
                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richards DE;
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                     DB 18; I
. 3.2e-08;
                                                                                                                                                                                                                                                                                                     Length 259;
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                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dwarf
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AAW38193
XX
AC AAW3
AC AAW3
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11-M
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T1-M
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CIOE
KW CIOE
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                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factors. SCR is expressed specifically in embryo root progenitor tissue and in certain root and stem tissues. It regulates a specific asymmetric division, and controls gravitropic response in aerial structures and root formation. SCR proteins (see ANW38178-201) from dicots and monocots, including SCR proteins lacking 1-4 of MOTIFS I-VI, and polypeptides corresponding to MOTIF I, II, III, IV, V or VI of SCR are claimed. Transgenic, plants can be engineered to overexpress the SCR protein, so that cell division is increased in roots, resulting in thicker root development, while a plant with an altered stem or hypocotyl gravitropism is less susceptible to lodging. Plants that contain an antisense molecule that suppresses the expression of endogenous SCR gene product have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of Arabidopsis SRPa2, a protein that shows homology to Arabidopsis SCARECROW (SCR) protein (see AAWA8178). SCR is a member of a novel protein family and contains number of functional domains similar to those found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding Arabidopsis SCARECROW protein - useful cell division and therefore alter root development, stem or hypocotyl gravitropism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      crop
                             Arabidopsis thaliana
                                                                       SCARECROW; SCR; SRPa8;
                                                                                                   Arabidopsis SCARECROW SRPa8
                                                                                                                                 11-MAY-1998
                                                                                                                                                              AAW38193;
                                                                                                                                                                                          AAW38193 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             thinner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 114-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-549683/50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-1997;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCARECROW; SCR; SRPa2; transgenic plant; root; gravitropism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                               314 CPYLKFAHFTANQAILEAF 332
                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                          improvement.
                                                                                                                                                                                                                                                                                                                                                                                                                            root development (all claimed).
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Wysocka-Diller J;
                                                                                                                                                                                                                                                                                                                                                                                                262 AA;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                (first entry)
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96US-0638617
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 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      / 100.0%; PJ
                                                                      transgenic plant; root; gravitropism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221pp; English.
                                                                                                   protein
                                                                                                                                                                                          277 AA
                                                                                                                                                                                                                                                                                                                                      Score 19;
; Pred. No.
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                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                      DB 18; I
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                                                                                                                                                                                                                                                                                                                                                    Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to modify plant or alter plant
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                                                                                                                                                                                                                                                                                                                       Gaps
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Misc-difference

269

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RESULT 10
AAW30795
ID AAW307
XX
AC AAW3(
XX
DT 19-)
XX
DE Ar7
XX
CHARLES ACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of Arabidopsis SRPa8, a protein that shows homology to Arabidopsis SCAREROROW (SCR) protein (see AAM38178). SCR is a member of a novel protein family and contains a number of functional domains similar to those found in transcription factors. SCR is expressed specifically in embryo root progenitor tissue and in certain root and stem tissues. It regulates a specific asymmetric division, and controls gravitropic response in aerial structures and root formation. SCR proteins (see AAM38178-201) from dicots and monocots, including SCR proteins (see AAM38178-201) from dicots and monocots, including SCR proteins (ase AAM38178-201) from dicots and monocots, including SCR proteins (see AAM38178-201) from dicots and monocots, including sCR proteins (ase AAM38178-201) from dicots and monocots, including sCR proteins (see AAM38178-201) from dicots and monocots, including sCR proteins (ase AAM38178-201) from dicots and monocots, while is increased in roots, resulting in thicker root development, while susceptible to lodging. Plants that contain an antisense molecule that suppresses the expression of endogenous SCR gene product have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                dwarf phenotype; lodging resistance; increased yield; flowering regulation; bolting inhibition; spinach; lettuce antibody; identification; probe; primer; antisense; sense;
                                                                                                                                                                                                                              Gibberellin insensitivity; gai-d3; plant growth inhibition;
                                                                                                                                                                                                                                                                                                                                                               19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW30795 standard; Protein; 282 AA
      Arabidopsis thaliana
                                                                                                     expression regulation; co-suppression; rice;
                                                                                                                                                                                                                                                                                              Arabidopsis thaliana gibberellin insensitivty gai-d3 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding Arabidopsis SCARECROW protein - useful to modify plant cell division and therefore alter root development, or alter plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N, Dilaurenzio L, Wysocka-Diller J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.0%; Score 19;
100.0%; Pred. No.
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. 3.4e-08;
ches 0;
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                                                                                                                                                                        lettuce;
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RESULT 11
AAG38577
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insensitivity (gai-d3) gene product (GAI-d3), the expression of which inhibits plant growth. However the inhibition is antagonised by gibberellin (GA), while gai expression confers a dwarf phenotype that is insensitive to GA. Manipulating gai-d3 and GAI-d3 cexpression can produce tall or dwarf plants, particularly the clatter for increased resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the cyceptative state until treated with GA, useful to inhibit bolting in spinach and lettuce. GAI-d3 can be used to raise specific antibodies for identifying homologous proteins or genes in other species. gai-d3 fragments can also be used as probes or primers to identify and clone related sequences, or in the preparation of cantisense or sense expression regulating (co-suppressing) sequences. Rice plants that express GAI-d3 may be resistant to Bakane disease. Manipulation of gai-d3 and GAI-d3 makes it possible to tallor the degree of dwarfism and GA sensitivity to particular crops
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 47612.
                                                                                                                                                                                               18-OCT-2000
                                                                                                                                                                                                                               AAG38577;
                                                                                                                                                                                                                                                          AAG38577 standard; Protein; 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Fig 6f; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding gibberellin inhibitor GAI and related antisense sequences - used to create tall, or particularly, plants, especially crops such as maize, rice and wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-415295/38
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                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or situations
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                                                                                                                                                                                                                                                                                                                                                                                                   19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is the Arabidopsis thaliana gibberellin
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                           Arabidopsis
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1 Similarity 100.0%; 1
19; Conservative 0;
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                                                                                                                                                              thaliana.
                                                                                                                                                                                                                                      thaliana protein
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                                                                               2000EP-0301439
99US-0121825.
99US-0123180.
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99US-0125788.
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J. 5.9e-08;
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99US-0145088. 99US-0145085. 99US-0145087.

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RESULT 13
AAB28575
ID AAB285
XX AAB285
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AC AAB285
DT 09-FEB
XX SCAREC
KW SCAREC
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COS AITALIS
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                                                              Benfey PN,
Helariutta
Scarecrow gene useful for producing transgenic plants expressing genes whose product increases starch, lignin or cellulose biosynthesis and confers herbicide, pathogen or insect resistance .
                                                                                                                                                                                                                           Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; SCL; transgenic plant; cell division; molecular marker; herbicide resistance; salt resistance; pathogen resistance; insect resistance.
                                           WPI; 2000-594315/56
                                                                                                                                        07-MAR-2000;
                                                                                                                                                               14-SEP-2000.
                                                                                                                                                                                   WO200053723-A2
                                                                                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                      Arabidopsis SCLa2.
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l Similarity 100.0%;
19; Conservative
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Pred. No.
                                                               Wysocka-Diller J,
J;
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thes 0;
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DY 19-P
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EW 61bb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is given in a specification relating to the Structure and function of a regulatory gene, SCARECROW (SCR).

SCARECROW-like (SCL) genes encoding proteins containing an amino acid sequence similar to the sequence of MOTIF III (VHIID) of Arabidopsis SCR protein are disclosed. SCR and SCL genes are useful for producing CC transgenic plants whose cell division is modified and root and/or stem CC development and gravitropism of stem or hypocotyl is altered. Cell division is increased or decreased in roots resulting in thicker or thinner root development. The transgenic plants are useful for expressing a gene of interest encoding a gene product that confers herbicide, salt, pathogen or insect resistance in root or embryos and genes encoding starch, lighin or cellulose biosynthesis in shoots. The SCR gene also CC confers less susceptibility to lodging in the transgenic plants than a wild-type plant. SCR gene sequences are also useful as molecular markers CC breeding of crop plants. 9. root or gravitropism trait in molecular CC breeding of crop plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
                                                                    Claim 1;
                                                                                                                              Nucleic acid encoding gibberellin inhibitor GAI and related antisense sequences - used to create tall, or particularly, plants, especially crops such as maize, rice and wheat
                                                                                                                                                                                                                                                                                                                                                                       Carol P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dwarf phenotype; lodging resistance; increased yield; flowering regulation; bolting inhibition; spinach; lettuce antibody; identification; probe; primer; antisense; sense;
The present sequence is the Arabidopsis thaliana gibberellin
                                                                                                                                                                                                                                                                WPI; 1997-415295/38.
N-PSDB; AAT91937.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (INNE-) INNES CENT INNOVATIONS LTD JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression regulation; co-suppression; rice; Bakane disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibberellin insensitivity; gai; plant growth inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09729123-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW30792 standard; Protein; 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana gibberellin insensitivty gai gene product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 19; Conserv
                                                                 Fig 4; 76pp;
                                                                                                                                                                                                                                                                                                                                                                Harberd NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531 AA;
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                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                Peng J,
                                                                                                                                                                                                                                                                                                                                                                    Richards DE
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insensitivity (gai) gene product (GAI), the expression of which inhibits plant growth. However the inhibition is antagonised by gibberellin (GA), while gai expression confers a dwarf phenotype that is insensitive to GA. Manipulating gai and GAI expression can produce tall or dwarf plants, particularly the latter for increased resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the vegetative state until treated with GA, useful to inhibit bolting in spinach and tettuce. GAI can be used to raise specific antibodies for identifying homologous proteins or genes in other species. gai fragments can also be used as probes or primers to identify and clone related sequences, or in the preparation of antisense or sense expression regulating (co-suppressing) sequences. Rice plants that express GAI may be resistant to Bakane disease. Manipulation of gai and GAI makes it possible to tailor the degree of dwarfism and GAI sensitivity to particular crops or situations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
                                                                                                                                                                                17-NOV-1999;
17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                          Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                         Plant transcription factor; phenotype; sugar sensing characteristic; transgenic plant; plant yield; growth; germination; photosynthesis; glyxylate metabolism; respiration; pathogen response; wounding resp cell cycle regulation; pigmentation; flowering; senescence; physiolo
Jiang C, Heard J,
Yu G, Samaha R;
                                                                                                             (HEAR/)
                                                                                                                                         (MEND-)
                                                                                                                                                                                                                                                                                               WO200135725-A1.
                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                            storage organ; metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE02545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE02545 standard; Protein; 532 AA.
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                                                                                                                                                                                                                                         14-NOV-2000; 2000WO-US31414
                                                                                                                                                                                                                                                                     25-MAY-2001.
                                          (SAMA/)
                                                                                                 (PILG/)
                                                                                    ADAM/)
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19; Conser
                                                                                 PILGRIM M.
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                                                                                                            MENDEL BIOTECHNOLOGY INC.
JIANG C.
HEARD J.
PINEDA O.
                                          SAMAHA R.
                                                                    RIECHMANN J
                                                         YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription factor G308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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2000US-0197899.
2000US-0227439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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              Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.0%;
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Pred. No.
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              Pilgrim M,
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6.le-08;
                Adam
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                Riechmann JL;
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                                             δÃ
                                                                                                                                                                                                                                                         The patent relates to polynucleotides encoding 35 plant transcription of factors which may be used to modify phenotype associated with a plant's of guar sensing characteristics and increasing yield when their expression of level is altered. Sugars are central regulatory molecules that control of each of physiology, metabolism and development. Therefore the cDNAs of the invention are useful for modifying the growth and of germination rates of plants, photosynthesis, glyoxylate metabolism, of response, wounding response, cell cycle regulation, pathogen of response, wounding response, cell cycle regulation, pigmentation, of lowering and senescence of plants and for modifying sink-source of lowering and senescence of plants, and other storage organs leading of the invention factor polynucleotides and conjupeptides may be used to alter the structure and developmental of characteristics of plants such as soybean, wheat, corn, potato, cotton, crice, oliseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, confice, cucumber, egaplant, grapes, honey dew, lettuce, mango, melon, conion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, of the present sequence is an Arabidones fruits and/or vegetable brassicas.
                                                                Query Match
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 74-76; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD06646.
                                                                                                                                                                                                                                              The present sequence is an Arabidopsis thaliana transcription factor.
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532 AA;
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100.0%; Pred. No. 6.1e-08;
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JC7219
E81408
E81408
T45525
S49886
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T101552
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S64439
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AF-9	AB(	pro	hyp	pro	91,	hy	Ľ-	L-1	unJ	myl	pro	mRI	hyp	hyp	hyp
AF-9 protein	transporter pe	robable membrane	ypothetical prote	protein kinase	lycerol-3-phospha	ypothetical prote	<pre>-ascorbate perox:</pre>	-ascorbate perox:	nknown protein Ti	yb-like protein	rotein F22C12.16	NA binding	ypothetical	nypothetical prote	pothetical

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C; Accession: G96688
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
A; Arthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
                                                                                                                                  RGA-like protein - Arabidopsis thaliana
N;Alternate names: protein K3M16.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51475
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tal submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
A;Accession: T51475
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T51475
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                                                       A; Molecule type: DNA
A; Residues: 1-523 <SAT>
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A; Experimental source: cultivar Columbia; BAC clone K3M16
                                                                                                         A; Status: preliminary
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A; Residues: 1-511 <STO>
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                              A; Cross-references: EMBL: AL391150
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: H86282
                                              A;Cross-references:
C;Genetics:
                                                                                                                                                                        A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487 A;Accession: D84426
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A; Map position: !
A; Note: K3M16_60
A; Gene: At2g01570
A; Map position: 2
                                                                                               A; Molecule type: DNA
A; Residues: 1-587 <ST
                                                                                                                                                                                                                                                 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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A; Residues: 1-533 <STO>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                   hypothetical protein At2g01570 [imported] - Arabidopsis thaliana (species: Arabidopsis thaliana (mouse-ear cress) C: Peb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 c: Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 c: Accession: D84426
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Best Local Similarity
Matches 19; Conserv
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                                                                     GB:AE002093; NID:g3785986; PIDN:AAC67333.1; GSPDB:GN00139
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Query Match

3.0%;

Score 19;

DB 2;

Length 587;

Yamaoka, T.; Moritani, M.;

Tanaka,

M.; Iwahana,

H.; Yoshimoto,

K.; Mi

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C;Species: Mus musculus (house mouse)
C;Date: 09-Jun-2000 #sequence_revision
C;Accession: JC7219
                                                                       RESULT
JC7219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
T04480
                                                    nuclear protein SR-25 - mouse
                                                                                                                                                                                                                                                                                                                A;Gene: MIPS:YOR382w
A;Map position: 15R
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S67261
A; Accession: S67294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Delius, H.; Hebling, U.; Hofmann, submitted to the Protein Sequence D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein YOR382w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein 06760
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: cdr29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-275 < GRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Grossi, M.; Gulli, M.; Stanca, A.M.; Cattivelli, plant Sci. 105, 71-80, 1995
A;Title: Characterization of two barley genes that
                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-153 <DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S67294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: T04480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acyl-CoA oxidase homolog - barley (fragment)
                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z75290; NID:g1420822; PID:e252449; PID:g1420823; GSPDB:GN000
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Hordeum vulgare (barley)
;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100 Matches 19; Conservative
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                                                                                                                                                 111 SSTSSSSSSSS 122
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be: cv. Arda, leaf
                                                                                                                                                                                                                 1.9%; bu
100.0%; Pr
'''' 0;
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Pred. No.
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Pred. No.
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                  09-Jun-2000 #text_change 21-Jul-2000
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hes 0;
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0.009;
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                                                                                                                                                                                                                                                         Length 153;
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probable periplasmic protein Cj0606 [imported] - Campylobacter jejuni (strain NCTC 11168 C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C;Accession: E81408
R;Parkhilli, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVllet, A.; Whitehead, S.; Barre Nature 403, 665-668, 2000
                                                                          C;Geneti
A;Gene:
                                                                                                                                                                                                                                                                                                                                                    WSC4 homolog [imported] - yeast (Kluyveromyces marxianus var. lactis) C;Specias: Kluyveromyces marxianus var. lactis, Candida sphaerica C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Jan-2000 C;Accession: T45525
                                                                                                                                                                 submitted to the EMBL Data Library, July 1999
A;Description: The ubiquitin-encoding genes of Kluyveromyces lactis.
A;Reference number: 223000
A;Accession: T45525
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-446 <BAO>
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A; Residues: 1-390 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: DDBJ:AB035383; NID:g7619895; PIDN:BAA94743.1; PID:g7619896 A;Experimental source: MIN6 cell line
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A; Residues: 1-229 < SAS>
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A; Title: Molecular cloning and expression analysis of a putative nuclear protein, A; Reference number: JC7219; MUID:20175222
A; Accession: JC7219
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                                                                                                                    A;Cross-references: EMBL:AJ243800; PIDN:CAB50897.1
A;Experimental source: strain 2359/152
                                                                                              Genetics:
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Best Local
    Query Match
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nes 12; Conserv
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nes 12; Conserv
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Pred. No.
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    12;
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. 0.013;
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0.02;
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  2;
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  Length 446;
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unknown protein F14G6.20 [imported] - Arabidopsis thaliana
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A;Gene: SGD:SIM1
A;Cross-references: SGD:S0001385; MIPS:YIL123w
A;Map position: 9L
C;Superfamily: Saccharomyces NCA3 protein
C;Keywords: transmembrane protein
C;Keywords: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
S49886
                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F26F4.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T16168
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T16168
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A; Residues: 1-475 <HAM>
A; Cross-references: GB:Z47047; EMBL:Z46833; NID:g603997; PID:g763223; MIPS:YIL123w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAPLEARCH MEMBRANE PROTEIN VIL123W - yeast (Saccharomyces cerevisiae)
NAPLEARCH NAMES: hypothetical protein YI8277.06
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jan-2000
C;Accession: S49886
                                                                                                                                                                A; Experimental source:
C; Genetics:
A; Gene: CESP:F26F4.6
A; Introns: 34/1
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A; Accession: S49886
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                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-164 < FUL>
                                                                                                                                                                                                                                                                                             A; Description: The sequence
A; Reference number: Z18471
A; Accession: T16168
A; Status: preliminary; tran
                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, March A; Description: The sequence of C. elegans {\bf A}
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Best Local Similarity
Matches 12; Conserv
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                                                                         Matches
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Best Local Similarity
Matches 11: Conserv
106
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                                  184 STSSSSSSSS 194
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STSSSSSSSS
                                                                                                                                                                                                                                                                                           preliminary; translated from
                                                                       11;
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                                                                         Conservative
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                                                                                                                                                                                                                       EMBL:U12964; NID:g1213452; PID:g529204; PIDN:AAA91221.1; CESP:F26
ce: strain Bristol N2
116
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                                                                                      1.8%;
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cosmid F26F4
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RTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wondowsone 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719
C;Accession: E96685
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
                                                                                           probable disease resistance protein F15E12.17 (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Graves, T.; Sutterer, C.; Hawkins, M.; Wilson, R. submitted to the EMBL Data Library, January 1998 A;Description: The sequence of C. elegans cosmid C3 A;Reference number: 221241 A;Accession: T32889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C34B2.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32B89
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A;Molecule type: DNA
A;Residues: 1-216 <STO>
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96794
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A;Experimental source: strain Bristol N2; clone C34B2
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A; Residues: 1-238 <GRA>
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A; Introns: 35/3; 91/2; 200/2
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Best Local Similarity 100.0%;
Matches 11; Conservative
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Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: E96685
                                                                                                                                                                                                                                                                                                                                                                                          R;Dempsey, S.; Harper, M. submitted to the EMBL Data Library, July 1997 A;Description: The sequence of A. thaliana TM018A10. A;Reference number: Z14348 A;Accession: T01552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein A_TM018A10.2 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
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A;Molecule type: DNA
A;Residues: 1-429 <STO>
A;Cross-references: GB:
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A;Residues: 1-575 <DEM>
A;Cross-references: EMBL:AF013294; NID:g2252848; PID:g2252850
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A; Introns: 271/3
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LYTE_BACSU
PLSB_PHAVU
KG3H_DICDI
YODO_YEAST
Y859_TREPA
YN23_YEAST
Y859_TREPA
YN23_YEAST
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YL78_YEAST
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YL71_CHICK
FIG2_YEAST
SUZ2_ASPFU
VIT1_AEDAE
HMEN_HELTR
108_LYCES
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RLA2_ASPFU
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                                                                                                                                                                                                                                                                                                                                                           arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
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B 24

183 SSTSSSSSSSS 194 ||||||||||| 182 SSTSSSSSSSS 193

Matches 183

12;

Conservative

0,

Mismatches

0;

Indels

0;

Gaps

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BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, BDNF, 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                               070183;
30-MAY-2000
30-MAY-2000
30-MAY-2000
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LHUMAN
YC18_HUMAN
STRAIN-HARTLEY WHITE; TISSUE-Liver;
Inoue M., Nakayama C., Noguchi H.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PROMOTES THE SURVIVAL OF NEURONAL POPULATIONS
ALL LOCATED EITHER IN THE CENTRAL NERVOUS SYSTEM OR DIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                   Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                                BDNF
                                                                                                                                                                                                                                                                                                                        BRAIN-DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BDNF_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Prediction of the coding sequence complete sequences of 100 for large proteins in vitro."; DNA Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20039619; PubMed=10574462;
Nagase T., Ishikawa K.-I., Kikuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL PROTEIN KIAA1218 KIAA1218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 SSTSSSSSSSS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSTSSSSSSSS 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB033044; BAA86532.1; -.
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12; Conserv
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223
652
786
786
864 AA;
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
ED NEUROTROPHIC FACTOR PRECURSOR (BDNF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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664
790
92138 .
                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences of unidentified human genes. XV 100 new cDNA clones from brain which code
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12;
Pred. No.
                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 255
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0.024;
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          OR DIRECTLY
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RESULT
YG3A_YK
TG3A_YK
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Best Local S
Matches 11
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ProDom; PD002052; NGF: 1.
SMART; SM00140; NGF: 1.
PROSITE; PS00244; NGF: 1: 1
PROSITE; PS50270; NGF=2: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YG3A_YEAST
P53278;
01-OCT-1996
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DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
CHAIN
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SGD; S0003362; YGR130C.
Hypothetical protein. T
DOMAIN 164 185
DOMAIN 205 218
                                                                                           EMBL; z72915; CAA97143.1; HSSP; P56255; lpJr.
                                                                                                                                                                                                                                                                                                                                        Nawrocki A., del Bino S., Goffeau A.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST
                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                van Dyck L., Skala J.,
Nawrocki A., del Bino S
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGR130C
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SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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137
149
194
204
129
255 /
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L 92.7
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255
255
216
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247
129
28308
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34,
34,
KDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetaceae;
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                de Wergifosse P.,
S., Goffeau A.;
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BY SIMILARITY.
BRAIN-DERIVED NEUROTROPHIC FACTOR.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

BY SIMILARITY.

N-LINED (GLCNAC. . .) (POTENTIAL).
MW; BA95BA3EBBBBFA04 CRC64;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ation update)
ASN2-PHB1 INTERGENIC REGION.
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0.063;
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POLY-SER.

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RESULT
MSP1_PI
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Best L
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                                                        CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
                                                                                          CARBOHYD
CARBOHYD
                                                                                                                 SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium berghei yoelii.
Eukaryota; Alveolata; Apic
NCBI_TaxID=5862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSP1_PLAYO P13828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLAYO
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88124889; PubMed=2448778;
Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.;
"The 3' portion of the gene for a Plasmodium yoelli merozoite surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSP-1
                                                                                                                                      Transmembrane;
                                                                                                                                                           EMBL; J03612; AAA29762.1; -.
EMBL; J04668; AAA29702.1; -.
PIR; A28121; A28121
PIR; A45532; A45532.
                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                  CARBOHYD
                                              CARBOHYD
                                                                                                                                                  Malaria;
                                                                                                                                                                                                                                                                                                                                                                                 antibody.
                                                                                                                                                                                                                                                                                                                                                                                              antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1093-1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis upstream of the gene encoding major merozoite surface antigens of Plasmodium you biochem. Parasitol. 39:285-288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lewis A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90205979; PubMed=2320061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PMMSA) (230 KDA).
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                                                                                                                                                                                                                                                                                                           PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTMEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U.S.A. 85:602-606(1988). SUBCELLULAR LOCATION: ATTACHED TO THE MEMBR
                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STSSSSSSSS
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11; Conser
                                                                                                                                                                                                                                                                                                                                                                                            encodes the epitope recognized
                                                                                                                                                Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apicomplexa; Haemosporida;
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                                          MEROZOITE SURFACE PROTEIN 1:
N-LINKED (GLONAC. .) (POTEN:
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N-LINKED
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CONFLICT
SEQUENCE
                                                                                                            PROSITE;
                                                                                                                                                                         EMBL; X92963; CAA63539.1;
HSSP; P15731; 2UCE.
MIM; 602916; -...
                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UBIQUITIN-CONJUGATING ENZYME E2-21 PROTEIN LIGASE) (UBIQUITIN CARRIER UBE2E1 OR UBCH6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
20-AUG-2001 (Rel. 40,
                                                               SEQUENCE
                                                                           BINDING
                                                                                                                                     Pfam; PF00179; UQ_con; 1
SMART; SM00212; UBCc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=96162027; PubMed=8576257;
Nubber U., Schwarz S., Kaiser P., Schneider R., Scheffne "Cloning of human ubiquitin-conjugating enzymes UbcH6 a (E2-F1) and characterization of their interaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=96162027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UBC6_HUMAN
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                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          <del>-</del>
                                                                                        DOMAIN
                                                                                                Obiquitin conjugation; Ligase; Multigene family.
                                                                                                                                                              InterPro; IPR000608; UBQ_conjugat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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 Local Similarity
nes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              AMP + PYROPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE. PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.
                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE AMP + PYROPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: CATALYZES THE COVALENT PROTEINS. MEDIATES THE SELECTIVE
                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING STRONGEST, TO DROSOPHILA UBCD2.
                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED
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                                                                                                           PS00183; UBIQUITIN_CONJUGAT_1; 1. PS50127; UBIQUITIN_CONJUGAT_2; 1.
                                                              131
193 AA;
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ilarity 100.0%;
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CATALYZES THE COVALENT ATTACHMENT C
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A; 197230
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21404 MW;
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Last annotation update)
ENZYME E2-21 KDA UBCH6
UITIN CARRIER PROTEIN).
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                          1.68;
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L -> V (IN REF. 2)
MW; 9A6291658EB0F4
           Score 10;
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Pred.
                                                              UBIQUITIN (BY SIMILARITY)
; 2FBC50BE2A6A0008 CRC64;
                                                                                        POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
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 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schneider R., Scheffner M.; ugating enzymes UbcH6 and UbcH7 their interaction with E6-AP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9A6291658EB0F45D CRC64;
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0.32;
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                         Length 193
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N OF SHORT-LIVED
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01-0CT-1996 (Rel. 34, Last squence update)
01-NOV-1997 (Rel. 35, Last annotation updat
UBIQUITIN-CONJUGATING ENZYME E2-21 KDA UBCH
                                                                                                                                                                                                        Ubiquitin conjugation; Ligase; Multigene family.
DOMAIN 9 18 POLY-SER.
                                                                                                                                                                                                                              PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; PROSITE; PS50127; UBIQUITIN_CONJUGAT_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96162026; PubMed=8576256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN). UBCH6 OR UBCM3 OR UBCE5.
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01-OCT-1996
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                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                             InterPro; IPR000608; UBQ_conjugat.
                                                                                             184 STSSSSSSSS 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.
MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR
UBIQUITIN-THIOLESTER FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LY AMP + PYROPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRONGEST, TO DROSOPHILA UBCD2
                                                                                                                                                                                                                                                                                          MGI:107411;
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                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                       requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                131
193 AA;
                                                                                                                      Conservative
             STANDARD;
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                                                                                                                                                                                                                                                                                          Ubce5
                                                                                                                                                                                131
21333 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Rodentia;
                                                                                                                                   100.0%;
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Pred. No.
                                                                                                                                                                                            UBIQUITIN (BY SIMILARITY).
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             PRT;
                                                                                                                                                                                 B535B3095EF6C445 CRC64;
                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ion update)
KDA UBCH6 (EC 6.3.2.19) (UBIQUITIN-
             246
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RA MAYDELNE-ZUUS-498; PUDDMGG-UD-L/198;
RA MAYOR KF.X. Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stlekema W., Ebtlan K.-D., Terryn N.,
RA Harris B., Alsorge W., Brandt P., Grivell L.A., Rleger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Weichselgartner M., Delseny W., Puigdomenech P., Watson M., Schmidtheini T.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Van der Schueren J., Grymonprez B., Gihang Y.-J. Vandenbussche F.,
RA Van der Schueren J., Grymonprez B., Gihang Y.-J. Vandenbussche F.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J. Vandenbussche F.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J. Vandenbussche F.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkse W.,
RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA De Keyser A., Bysyshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Clark L., Doggert J., Hall S., Kay M., Lennard N., McLay K., Wayes R.,
RA Clark L., Doggert J., Hall S., Kay M., Lennard N., McLay K., Wayes R.,
RA Glark L., Doggert J., Rattlann B., Granderath K., Danner D., Herzl A.,
RA Petter D., Holts M., Fartmann B., Granderath K., Danner D., Herzl A.,
RA Glark L., Schwarz S., Scholler P., Hense V., Rechmann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Glabons T., Weber N., Vandenbol M., Bargues M., Ferncs P., Beleke C.,
RA Glabons T., Weber N., Vandenbol M., Bargues M., Ferncs P., Beleke C.,
RA Glabons T., Weber N., Vandenbol M., Bargues M., Ferncs P., Beleke C.,
RA Frishman D., Haase D., Lencke K., Mewes H., M., Beber S., Francs P., Bleike C.,
RA Frishman D., Haase D., Lencke K., Mewes H., Mustler L.,
RA Latteille P., Couttney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Latteille P., Schmidt W., Jenter M., Stocker S.,
RA Percor P.,
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
AUXIN-RESPONSIVE PROTEIN IAA11 (INDOLEACETIC ACID-INDUCED PROTEIN IAA11 OR AT4628640 OR T5F17.90.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheog Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abel S., Nguyen M.D., Theologis A.; "The PS-IAA4/5-like family of early Arabidopsis thaliana.";
                                                        Nature 402:769-777(1999).
-!- FUNCTION: COULD ACT AS REGULATOR OF MEDIATING THE VARIOUS AUXIN-INDUCED
                                                                                                                    "Sequence and analysis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20083488; PubMed=10617198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                     GROWTH (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=7658471;
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                                                          GENES F
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                                                            RESPONSIBLE FOR
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RESULT 9
LYTE_BACSU
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Best Local S
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P54421;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE ENDOPEPTIDASE LYTE PRECURSOR (PHOSPHATASE-ASSOCIATED PROTEIN
PAPQ) (CELL WALL-ASSOCIATED POLYPEPTIDE CWBP33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
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Multigene family; Nuclear protein; Translation regulation.
DOMAIN 57 67 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U18413; AAC49052.1; -. EMBL; L161573; CAB81452.1; -. EMBL; A11727; Arath;1524;7127. Mendel; 7127; Arath;1524;7127. InterPro; IPR003311; AUX_IAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                       J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                          genes."
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MEDLINE=94321340; PubMed=8045898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Margot P., Wahlen M., Gholamhuseinian "The lytE gene of Bacillus subtilis 10 hydrolase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98117063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-168
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                       the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                             Jin S., Somenshein A.L.;
"Identification of two distinct Bacillus subtilis citrate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 311-334 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 180:749-752(1998)
                                                                                                                                                                                                                         FUNCTION: PUTATIVE D-GLÜTAMATE - M-DIAMINOPIMLATE ENDOPEPTIDASE. CELL WALL HYDROLASE INVOLVED IN CELL AUTOLYSIS. SUBCELLULAR ILOCATION: CELL-WALL BOUND.

DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN
                                                                                                                                                            SIMILARITY:
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                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                         176:4669-4679(1994).
                                                                                                                                                          BELONGS TO THE E.COLI NLPC CONTAINS 3 LYSM REPEATS.
a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9457885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26516 MW; 449054E312FBBDAD CRC64;
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Pred. No.
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. 0.44;
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                                                                                                                                                                                    / LISTERIA P60 FAMILY
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                  Usage
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RESULT 10
PLSB_PHAVU
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Best Local Similarity
Matches 10; Conser
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SubtiList; BG11406; lyte.
InterPro; IPR002482; Lysm.
InterPro; IPR000064; NLPC_P60.
Pfam; PF00476; Lysm; 3.
Pfam; PF00877; NLPC_P60; 1.
SMARP; SM00257; Lysm; 3.
                                                                                                                                                                                                                                                                                                                                    Q43822;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR
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DOMAIN
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; eudicotylo
eurosids I; Fabales; Fabaceae; Papilion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U38819; AAC25975.1; -
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                                                                                                                                                                                                                                  STRAIN=CV. ANNABEL; TISSUE=Leaf; MEDLINE=95232196; PubMed=7716242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         NCBI_TaxID=3885;
                                                                                                                                                                                                                                                                                                                Phaseolus vulgaris (Kidney bean) (French bean)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            132
                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 STSSSSSSS 193
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28
88
151
73
132
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193
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LYSM 3.
POLY-SER.
POLY-SER.
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MSAT
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Pred. No.
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POLY-SER.
D809C7DD4BAC475D
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                                                                                                                                                                                                                                                                                   eptophyta; Embryophyta; Trache
  eudicotyledons; core eudicots
; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                         461
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0.57;
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                                                                                                                                                                                                                                                                                             a; Tracheophyta;
eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                     2.3.1.15) (GPAT).
                                                           a collaboration
                                                                                                                                                                                                                                                                                    Phaseolus.
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RESULT
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Best Local
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 Phosphorylation.

DOMAIN 57

NP_BIND 63

BINDING 86

ACT_SITE 180

MOD_RES 215

DOMAIN 23

DOMAIN 29

DOMAIN 405

DOMAIN 405

DOMAIN 429

DOMAIN 429

DOMAIN 456
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P51136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
SEQUENCE
                                                                                                                                                                                                                     DictyDb; DD01073; gskA.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_kin_actsite.
Pfam; PF00059; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95112340; PubMed-7813009;
Harwood A.J., Plyte S.E., Woodgett J., Strutt H., Kay R.R.;
"Glycogen synthase kinase 3 regulates cell fate in Dictyostelium.";
Cell 80:139-148(1995).
-1- FUNCTION: DURING CELLULAR DIFFERENTIATION IT MAY MEDIATE A CAMP
STIMULATED SIGNAL TRANSDUCTION PATHWAY THAT REGULATES PRESPORE J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
GLYCOGEN SYNTHASE KINASE-3 HOMOLOG (EC 2.7.
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Phospholipid biosynthesis; Transferase; Acyltransferase;
Transit peptide; Chloroplast.
TRANSIT 1 96 CHLOROPLAST (POTENTIAL).
                                                                                                                                                                  PROSITE; PS00108; PROTEIN_KINASE_ST; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                             PROSITE; PS00107;
                                                                                                                                                        Fransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 SSTSSSSSSS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                                                                                                                                                                                                                                                                                                              PRESTALK B CELL PROPORTIONS.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES CDC2/CDKX SUBFAMILY; GSK-3 SUBSUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSTSSSSSSS 58
                                                                                                                                                                                                                                                                             L34674; AAA65968.1;
P24941; 1AQ1.
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                                                                                                                                                                                                              SM00220;
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10; Conser
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97
461 AA;
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                                                                                                                                                  Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                           S_TKc; 1.
                                                                                                                                                                                              PROTEIN_KINASE_ATP;
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50697 MW;
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (BY SIMILARITY).
POLY-THR.
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POLY-SER.
POLY-SER.
POLY-THR.
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GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE; EAC4FC837908B38A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10;
Pred. No.
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(EC 2.7.1.-) (GSK-3).
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Best Local
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Q08193;
Q1-NOV-1997
Q1-NOV-1997
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its the EMPL of the EMPL of the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
SIGNAL
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Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. SIMILARITY: BELONGS TO THE GAS1 FAMILY.
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35, Last sequence update)
35, Last annotation update)
KDA PROTEIN IN MSEI-LAG2 INTERGENIC REGION
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403
460
427
439
500
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POLY-SER.
N-LINKED (GLCNAC. . .) (POT
                                                                                                                                                                                                                                                               Score 10;
; Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL ASP/GLU-RICH
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0.75;
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(HIGHLY
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RESULT 14
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P53832;
01-OCT-1996
01-OCT-1996
15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C.M., Noris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 281:375-388(1998).
-!- SIMILARITY: BELONGS TO THE UPF0164 FAMILY.
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION. REF.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treponema pallidum.
Bacteria; Spirochaetales;
                                                    Messenguy F., Dubois Glansdorff N.;
                                                                                                                     Eukaryota; Fungi; !
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome spirochete.";
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                          Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases -i- SIMILARITY: TO S.POMBE SPBC3D5.14C.
                                                                             SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                             YNL283C OR N0583
                                                                                                                                                                         PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein;
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494 AA;
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(Rel.)
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36,
KDA
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52883 MW;
                                                                                                                     Saccharomycetaceae;
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Pred. No.
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                                                                                                                     Saccharomyces.
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produced through a collaboration
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Best Local
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          MS2P_HUMAN STANDARD; PRT; 519 AA.
043462;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
STEROL-REGULATORY ELEMENT-BINDING PROTEINS INTRAMEMBRANE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                         MEDLINE=98324087; PubMed=9659902;
Rawson R.B., Zelenski N.G., Nijhawan D.
Chang T.Y., Brown M.S., Goldstein J.L.;
"Complementation cloning of S2P, a gene
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002889; WSC. Pfam; PF01822; WSC; 1. SMART; SM00321; WSC; 1.
                 between
                              This
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metalloprotease required for intramembrane
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                                                                                                                                                                                                                                                                             TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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                                                              TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, MUSCLE, KIDNEY AND PANCREAS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50 (Z.
                                                                                          BINDING PROTEINS (SREBPS) WITHIN THE FIRST TRANS
THEREBY RELEASING THE N-TERMINAL SEGMENT WITH A
TRANSMEMBRANE SEGMENT ATTACHED. SITE-2 CLEAVAGE
CLEAVAGE WHICH TAKE PLACES IN THE LUMENAL LOOP.
COFACTOR: BINDS ONE ZINC ION (POTENYIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, P
                                                                                                                                                                                    Cell 1:47-57(1997).
FUNCTION: INTRAMEMBRANE PROTEOLYSIS OF STEROL-REGULATORY ELEMENT-
                                                      METALLOPROTEASE).
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WOT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation Bioinformatics Institute. There are no restrictions
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Search completed: January 22, 2002, 16:37:08 Job time: 318 sec
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MEROPS; M50.001; -.

INTERPO; IPR001193; Peptidase_M50.

INTERPO; IPR001193; Peptidase_M50; I.

Pfam; PF02163; Peptidase_M50; 1.

PRINTS; PR01000; SREBPS2PTASE.

PROSITE; PS00142; ZINC_PROTEASE; I.

PROSITE; PS00142; ZINC_PROTEASE; I.

STANCE (CATALYTIC) (BY SIMILARITY).

ACT_SITE 172 172 BY SIMILARITY.

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128 SSSSSSSSL 137
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519 AA;
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Q08906 saccharomyc
Q9jm93 mus musculu
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P91720 drosophila	P91720	თ	614	1.8	11	44
Q90237 anolis pulc	Q90237	13	600		11	43
O23083 arabidopsis	023083	10	575	1.8	11	42
	Q9DA19	11	450		11	41
Ç,	Q9C515	10	429	1.8	11	40
Q9xyq7 lytechinus	Q9XYQ7	ъ	417	1.8	11	39
Q9fn34 arabidopsis	Q9FN34	10	371	1.8	11	38
ο.	Q9W3Z5	σı	321	1.8	11	37
	Q9S782	10	318	1.8	11	36
Q9m160 arabidopsis	Q9M160	10	291	1.8	11	35
a	044958	σı	238	1.8	11	34
Q9c9j8 arabidopsis	Q9C9J8	10	216	1.8	11	33
	Q99NV1	1	193	1.8	11	32
Q99nv0 hydrochoeru	Q99NV0	11	187	1.8	11	31
O	Q19817	υ	164	1.8	11	30
Q9dh52 meleagrid h	Q9DH52	12	2164	1.9	12	29
Q9elfl meleagrid h	Q9E1F1	12	2161	1.9	12	28
089232 canine herp	089232	12	1383	1.9	12	27
O15025 homo sapien	015025	4	1297		12	26
	Q9W2S4	Çī	989	1.9	12	25
Q9gz10 drosophila	Q9GZ10	υı	856		12	24
Q9btq8 homo sapien	8QTEQ	4	574		12	23
Q9y849 kluyveromyc	Q9Y849	w	446		12	22
	Q9HED2	ω	409	1.9	12	21
Q9phr0 campylobact	Q9PHR0	Ν	390	1.9	12	20

## ALIGNMENTS

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Best Local Similarity
Matches 623; Conserv
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SEQUENCE FROM N.A.

MEDLINE=99347734; PubMed=10421366;

Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,

Peng J., Richards D.E., Fish L.J., Worland A.J., Pelica F.,

Flintham J.E., Beales J., Fish L.J., Worland A.J., Harberd N.P.;

Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;

Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ST59;
Q9ST59;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                             modulators.";
Nature 400:256-261(1999).
EMBL; AJ242531; CAB51555.1; --
SEQUENCE 623 AA; 65337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIBBERELLIN RESPONSE MODULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHT-DlA.
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   121
                121 QLNASTSSTYTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRDPKRMRT 180
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                                                                                                                                        1 MKREYQDAGGSGGGGGGGGSSEDKMMYSAAAGEGEEVDELLAALGYKVRASDMADVAQKL
QLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAGATAPADLSADSVRDPKRMRT
                                                                             EQLEMAMGMGGVGÆGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPPPLPPAP 120
                                                                                                                          MKREYQDAGGSGGGGGGGGSSEDKMMVSAAAGEGEEVDELLAALGYKVRASDMADVAQKL
                                                             EQLEMAMGMGGVGAGAAPDDSFATHLATDTVHYNPTDLSSWVESMLSELNAPPPPLPPAP
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               623 AA
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SEQUENCE FROM N.A.

MEDLINE-99347734; PubMed=10421366;

MEDLINE-99347734; PubMed=10421366;

Meng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M., Fintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F., Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;

Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;
                                                                                                                                                                                                                                                                                                                                                                                                       Q9ST48;
Q9ST48;
01-MAY-2000
01-MAY-2000
01-MAR-2001
01-MAR-2001
                                                                                                                                                                     EMBL; AJ2
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Str. Spermatophyta; Magnoliophyta; Panicoldeae; Andropogoneae; Z.
                                                                                                                                                                                                                                                                                                                                                                Zea mays (Maize).
Eukaryota; Viridiplantae;
                                                                                                                                                                     Nature 400:256-261(1999).
EMBL; AJ24230; CAB5157.1; -.
EMBL; AJ24230 630
NON_TER 630 630
SEQUENCE 630 AA; 66028 MW;
    362
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                                                                                                                   Local Similarity
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ALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKLAQFAHTIRVDFQYRGLVAATL
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                                                               PDSSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEAFAGCRRVHVVDFGIKQGMQWP
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation updat
RESPONSE MODULATOR (FRAGMENT).
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                   21.2%;
100.0%;
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yta; Liliopsida; Poales; Poaceae; PACC cl
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                                                                                                       0;
                                                                                                                   Score 132; DB 10;
Pred. No. 1.8e-115;
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Best Local
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01-MAY-2000 (TrEMBL:
01-MAY-2000 (TrEMBL:
01-MAY-2000 (TrEMBL:
RGA1-LIKE PROTEIN:
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Q9MB96;
01-OCT-2000
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Gukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Be Bowman C.L., White O., Nerman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III BAC T21P5 genor Submitted (OCT-1999) to the EMBL/GenBank/DDJ databe EMBL, AC009895; AAR01590.1; -
                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 245:21-29(2000)
EMBL; AB030956; BAA9
SEQUENCE 625 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
MEDLINE-20179680; PubMed=10713441;
Ogawa M., Kusano T., Katsumi M., Sano H.;
"Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog," osga "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog," osga "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog," osga "Rice gibberellin-insensitive gene homolog, OsGAI, encodes a "Rice gibberellin-insensitive gene homolog," osga "Rice gibberellin-insensitive gene gibberellin-insensitive gene gibberellin-insensitive gibberellin-insensitive gibberellin-
                                                                                                                                                       STRAIN-CV. COLUMBIA;
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AA; 65406 M
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b; Pred. No. 5.6
0; Mismatches
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Last sequence update)
Last annotation updat
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      CRC64;
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Query

Match

Score

23;

DB

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Length

Best Local Similarity

100.

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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Liam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Q9C8Y3;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                             065367;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 408:816-820(2000).
EMBL; AC020665; AAG52171.1; -.
SEQUENCE 511 AA; 56754 MW;
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l Similarity 100.0%;
22; Conservative
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
REGULATORY PROTEIN, PUTATIVE.
                                                                                                                                                                                                                           (TrEMBLrel. (TrEMBLrel.
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17,
                                                          Brassicaceae; Arabidopsis
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0; Mismatches
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thes 0;
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6e-12;
                                                                               Embryophyta; Tracheopedons; core eudicots;
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RESULT
Q9LF53
ID Q9LF53
AC Q9

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Best Local Similarity
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Best Local
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                                                                                       O9LF53;
Q9LF53;
01-OCT-2000 (Tremi
01-OCT-2000 (Tremi
01-OCT-2000 (Tremi
RGA-LIKE PROTEIN.
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01-JUN-2001 (TrE
01-JUN-2001 (TrE
01-JUN-2001 (TrE
PUTATIVE OSGAI.
P0707D10.30.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryospermatophyta; Magnoliophyta; eudicotyledons;
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PROSITE; PS502082; WD_REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_REGION;
Repeat; WD repeat.
SEQUENCE 662 AA; 73126 MW; 958AB;
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Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae;
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mendel; 29006; Arath; 3051; 29006.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 1.
                                                                        K3M16_60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone:P0707D10."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
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Ehrhartoideae;
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STRAIN-CV. COL-0;
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                                                                                                                                                                                                                                                                                                             163
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Oryzeae; Oryza
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51864 MW; 5FDB670EB8899492 CRC64; /
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                                                                                                              15,
15,
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(GA3) genomic
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yta; Liliopsida; Poales; Poaceae;
                                                                                                            Created)
Last sequence up
Last annotation
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Last annotation update)
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Pred. No.
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Pred. No.
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3.9e-09;
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7.6
      Embryophyta; Tracheophyta; edons; core eudicots; Rosid
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O23643; 01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
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023724;
01-JAN-1998
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01-MAY-2000
GAI PROTEIN.
                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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"Sequence and characterization of two Arabidopsis thaliana cDNAs
isolated by functional complementation of a yeast gln3 gdh1 mutant.";
EEBS Lett. 410:213-218(1997).
EMBL, Y11337; CAA72178.1;
Mendel; 24146; Arath;3051;24146.
SEQUENCE 532 AA; 58789 MW; 17AC719CA8072239 CRC64;
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MEDLINE-97379310; PubMed-9237632;
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Eukaryota; Viriddiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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57326 MW; 0F6CE0BD13403C35 CRC64;
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AC006917; AAF79228.1; -. 6464B8C129D79528 CRC64;
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MEDIJINE-98051192; PubMed-9389651;

Peng J., Carol P., Richards D.E., King K.E., Cowling R.J.,

Murphy G.P., Harberd N.P.;

"The Arabidopsis GAI gene defines a signaling pathway that negatively

regulates gibberellin responses.";

Genes Dev. 11:3194-3205(1997).

Genes Dev. 11:3194-3205(1997).

EMBL; Y15193; CAA75492.1; -.

Mendel; 24070; Arath;3051;24070.

SEQUENCE 532 AA; 58789 MW; 4AF4BC6EC4265503 CRC64;
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Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M., Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F., Hulzar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;

"Genomic sequence for Arabidopsis thaliana BAC F1086 from Chromosome
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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O1-JAN-1998 (TrEMBLrel. 05,

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EMBL; Y11336; CAA72177.1; -
Mendel; 24145; Arath; 3051;24145.
SEQUENCE 587 AA; 64023 MW; DOA7A3C741FB51EF CRC64;
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Truong H.N., Caboche M., Daniel-Vedele F.;
"Sequence and characterization of two Arabidopsis thaliana cDNAs
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phy G.P., Harberd N.P.;
phy G.P., Harberd N.P.;
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JL; Y15194; CAA75493.1; -
ndel; 24071; Arath;3051;24071.
OURNCE 587 AA; 64006 MW; F6F6C7738EE7DCA9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
19; Conser
                                                                                               Conservative
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Niterman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
Nature 402:761-768(1999).
EMBL; AC005560; AAC67333.1;
EMBL; AC005560; AAC67333.1;
EMBL; AC00550; AAC67333.1;
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Q43476;
Q1-NOV-1996;
Q1-NOV-1996;
Q1-JUN-2001;
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Q9SLH3;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PUTATIVE RGA1, GIBERELLIN REPSONSE MODULATION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-GREE GROSSI M., Gulli M., Stanca Grossi M., Gulli M., Stanca Plant Sci. 105:71-80(1995).
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SEQUENCE FROM N.A.
COLUMBIA;
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EMBL; X84055; CAA58874.1; -.
Mendel; 12863; Horvu; 2063;12863.
InterPro; IPR002655; ACOX.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                          Pfam; Pf01756; ACOX; NON_TER 1 SEQUENCE 275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
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                                                                                                                                                 16;
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19; Conservative
                                                                                                                                                                                Similarity
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(TIEMBLrel. 01, Last sequence update)
(TIEMBLrel. 17, Last annotation updat
CYL COA OXIDASE HOMOLOGOUS (FRAGMENT).
                                                                                                                                             Conservative
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yta; Liliopsida; Poales; Poaceae; Pooidea
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Search completed: January 22, 2002, 16:36:44 Job time: 344 sec

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 protein search, using sw model
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Match
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-09-117-853-4
US-09-117-853-4
US-08-861-464-14
US-08-89-6001-14
US-09-323-433A-14
US-09-196-525-3
US-09-196-525-3
US-08-545-860D-30
PCT-08-545-860D-30
PCT-08-785-310A-6
US-08-785-310A-6
US-08-66-344-43
S206152-12
S496550-6
US-08-08-08-208-90
US-08-08-08-96-344-43
S206152-12
S496550-6
US-08-08-08-90-90
US-09-005-069-90
US-09-005-069-90
US-09-005-069-90
US-09-005-069-90
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US-08-506-553C-8
US-08-506-553C-23
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       Sequence 6, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 43, Appli
Sequence 90, Appli
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US-09-117-853-8 US-09-117-853-8 ; Sequence 8, Application US/09117853 ; Patent No. 6307126 ; GENERAL INFORMATION: ; APPLICANT: Harberd, Nicholas P APPLICANT: Peng, Jinrong ; APPLICANT: Richards, Donald E ; TITLE OF INVENTION: Nucleic acid encoding GAI gene of ; FILE REFERENCE: 620-45 ; CURRENT APPLICATION NUMBER: US/09/117,853 ; CURRENT FILING DATE: 1998-08-12 ; EARLIER APPLICATION NUMBER: PCT/GB97/00390 ; EARLIER FILING DATE: 1997-02-12	Query Match 3.0%; Score 19; DB 4; Leng Best Local Similarity 100.0%; Pred. No. 4.4e-09; Matches 19; Conservative 0; Mismatches 0; I  Oy 314 CPYLKFAHFTANQAILEAF 332	US-09-117-853-6  US-09-117-853-6  Sequence 6, Application US/09117853  Patent No. 6307126  GENERAL INFORMATION: APPLICANT: Harberd, Nicholas P APPLICANT: Herberd, Jinrong APPLICANT: Richards, Donald E TITLE OF INVENTION: Nucleic acid encoding GAI gene of FILE REFERENCE: 620-45  CURRENT APPLICATION NUMBER: US/09/117,853  CURRENT FILING DATE: 1998-08-12  EARLIER APPLICATION NUMBER: PCT/GB97/00390  EARLIER APPLICATION NUMBER: GB 9602796.6  EARLIER FILING DATE: 1996-02-12  NUMBER OF SEQ ID NOS: 12  SOFTWARE: Patentin Ver. 2.0  SEQ ID NO 6  LEBNOTH: 259  TYPE: PRT ORGANISM: Arabidopsis thaliana US-09-117-853-6	ALIGNMENTS	28 9 1.4 218 4 US-09-068-655-7 29 9 1.4 246 4 US-09-185-160-7 30 9 1.4 262 1 US-08-186-81-6 31 9 1.4 275 3 US-08-186-853-20 32 9 1.4 285 3 US-08-861-661-4 34 9 1.4 285 4 US-09-318-661-2 35 9 1.4 300 3 US-09-318-661-2 36 9 1.4 300 3 US-08-765-856-2 37 9 1.4 300 3 US-08-765-856-2 38 9 1.4 302 3 US-08-765-856-4 39 9 1.4 302 3 US-08-765-856-4 39 9 1.4 302 3 US-08-651-136C-22 40 9 1.4 310 3 US-08-651-136C-22 41 9 1.4 322 1 US-08-61-136C-22 42 9 1.4 322 1 US-08-486-809-3 43 9 1.4 322 2 US-08-486-809-3 44 9 1.4 345 2 US-08-486-809-3 45 9 1.4 360 3 US-08-899-437-7
0	Length 259; ; ; Indels 0; Gaps 0;			Sequence 7, Appli Sequence 6, Appli Sequence 26, Appli Sequence 27, Appli Sequence 37, Appli

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CURRENT APPLICATION NUMBER: US/09/117,853
CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION UNMBER: PCT/GB97/00390
EARLIER FILING DATE: 1997-02-12
EARLIER APPLICATION UNMBER: GB 9602796.6
EARLIER FILING DATE: 1996-02-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
Thes 19; Conserve
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             GENERAL INFORMATION:
APPLICANT: Harberd, Nicholas P
APPLICANT: Peng, Jinrong
APPLICANT: Carol, Pierre
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI gene of Arabidopsis thaliana
FILE REFERENCE: 620-45
CURRENT APPLICATION NUMBER: US/09/117,853
CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: PCT/GB97/00390
EARLIER APPLICATION NUMBER: GB 9602796.6
EARLIER APPLICATION NUMBER: GB 9602796.6
EARLIER FILING DATE: 1996-02-12
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APPLICANT: Harberd, Nicholas P
APPLICANT: Peng, Jinrong
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI gene of Arabidopsis thaliana
FILE REFERENCE: 620-45
                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09117853
Patent No. 6307126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 8
LENGTH: 282
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NUMBER OF SEQ ID NOS: 12
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TYPE: PRT
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100.0%; Pred. No. 4.8e-09
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; Pred. No.
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Query Match
Best Local Similarity
Watches 12; Conserve
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Best Local Similarity
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/396,001
FILING DATE: 28-FEB-195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09351
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,408
FILING DATE: 16-AUG-193
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Guarente, Leonard P. APPLICANT: Austriaco Jr., Nicanor APPLICANT: Kennedy, Brian TITLE OF INVENTION: Genes Determinant of Invention: in Yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                 TELEPHONE: 781-861-6240
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CURRENT APPLICATION DATA:
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                                                                                                                                                LENGTH:
TYPE: a
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                                                                                                                                                                                                  TELEPHONE: 781-00:
                                                                                                                                                                                                                                                              NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6408A2Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 22-MAN CLASSIFICATION: 43
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Lexington
                                                                                                                                  TOPOLOGY:
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5874210
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             Conservative
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                                                                                                                                  linear
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100.0%; Pr
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             1.9%; Score 12; DB 2; Length 475; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
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Pred. No.
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0.00011;
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183 SSTSSSSSSSSS 194

SSTSSSSSSSSS 193

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US-09-323-433A-14

; Sequence 14, Application US/09323433A

; Patent No. 6218512
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                                                                                                                                                      GENERAL INFORMATION:
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Best Local Similarity
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                                                                   APPLICANT:
APPLICANT:
APPLICANT:
              APPLICANT: Kennedy, Brian
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: YEAST
FILE REFERENCE: 0050.1491-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14:
FILE REFERENCE: 0050.1491-003
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APPLICANT:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/396,001
FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6408A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Mili
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                                                                                 Austriaco Jr., Nicanor
Claus, James J.
Cole, Francesca
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                                                                                                                                                                                                                                                                                                                                             Conservative
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100.0%; Pred. No.
                                                                                                                                      Leonard P.
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SEQ ID NO 14
                                                                                                                                                           Sequence 3, Application US/08679765 Patent No. 5840866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Caról, Pierre
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI gene of Arabidopsis thaliana
FILE REFERENCE: 620-45
CURRENT APPLICATION NUMBER: US/09/117,853
CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: PCT/GB97/00390
EARLIER FILING DATE: 1997-02-12
EARLIER APPLICATION NUMBER: GB 9602796.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                   GENERAL INFORMATION:
AN-YOUNG, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillnan, Jennifer L.
APPLICANT: Hillnan, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN UBIQUITIN-CONJUGATING ENZYME NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 08/396,001
PRIOR FILING DATE: 1995-02-28
PRIOR APPLICATION NUMBER: PCT/US94/09351
PRIOR FILING DATE: 1994-08-15
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR FILING DATE: 1993-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1996-02-12
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Harberd, Nicholas P
APPLICANT: Peng, Jinrong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 16
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 475
                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 SSTSSSSSSSSS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 SSTSSSSSSSSS 193
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3174 Porter Drive
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100.0%;
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Pred. No.
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0.014;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

IBM Compatible

COUNTRY: U ZIP: 94304

U.S.

CITY: Palo Alto STATE: CA

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US-08-679-765-3
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US-09-196-525-3
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,7
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: pept:
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1064914
                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer
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LENGTH: 193 amino acids
                                                                                 APPLICATION NUMBER: US/09/196,525
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN UBIQUITIN-CONJUGATING
TITLE OF INVENTION: ENZYME
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                          APPLICATION NUMBER: 08/679,765
FILING DATE:
ITTORNEY/AGENT INFORMATION:
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CITY: Palo Alto
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OPERATING SYSTEM:
NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
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Pred. No.
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US-09-318-317-3

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LIBRARY: GenBank

CLONE: 1064914
US-09-196-525-3
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Best Local Similarity
Watches 10; Conserva
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                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Au-Young, Charles APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: HILLMAN UBIQUITIN-CONJUGATING
IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 1064914
                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                 FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
NIMBER: 36,749
                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 STSSSSSSSS 193
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CITY: Palo Alto
STATE: CA
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                                                          TOPOLOGY:
                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/318,317
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                                                                                                    LENGTH:
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3174 Porter Drive
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Pred. No.
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148 TSSSSSSSS 157

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; MOLECULE TYPE: protein US-08-320-559-30
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Best Local
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                                                 Best Local Similarity 100. Matches 10; Conservative
                                                                                 Query Match
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                                                                                                                                                                                                                                TELEFAX: (215) 568-3439
NFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-0CT-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAX-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 14 MAY 1
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
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185 TSSSSSSSSS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                   NAME: DeLuca, Mark
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                                                 %; Score 10; DB
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0; Mismatches
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Pred. No.
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1;
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                                                                               Length 568;
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RESULT 13
US-08-545-860D-30
US-08-545-860D-30
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                                                                                 TELEFAX: (215) 568-343
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION DATE: 19-OCT-1994
                                                                                                                                       REFERENCE/DOCKET NUMBER: TJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/971,094
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
ADDITIONATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Canaani,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                MOLECULE TYPE:
                                                                                                                                                                                                                                FILING DATE: 11-DEC-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/888,839 FILING DATE: 27-MAY-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/
FILING DATE: 22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 07-MAR-1996
                                                    TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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CITY: Philadelphia
                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                  568 amino acids
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SYSTEM: PC-DOS/MS-DOS
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               protein
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11-DEC-1991
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                                                                                                                          568-3439
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Query Match Best Local Similarity

1.6%;

Score 10; Pred. No.

DB 3; 1;

Length 568;

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                                                                                                                                                                       Sequence 5, Application US/08785310A Patent No. 5840532
GENERAL INFORMATION:
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Best Local Similarity 100
Matches 10; Conservative
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INFORMATION FOR SEQ ID NO: 30:
        APPLICANT: MCKNIGht, Steven L.
APPLICANT: MCKNIGht, Steven L.
APPLICANT: MCKNIGHT, David W.
TITLE OF INVENTION: Meuronal PAS Domain Protein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 568 amino acid
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100.0%; Pred. No.
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Search completed: January 22, 2002, 16:30:53 Job time: 273 sec
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                                                                                                                                                 Matches
                                                                                                                                                               Query Match 1.6%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4342
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                  186 SSSSSSSSS 195
                                                                                  214 SSSSSSSSS 223
                                                                                                                                                                                                                                                                                                     LENGTH:
TYPE: a
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Result No.

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Match Query

Length

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Description

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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                     Word size :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TOURNAL FEATURES SOURCE	AX005805 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS		444	2 42 4 2 2 F	40	ມ ເມ ວ 80	36 37	3 5 A	ιω ( ω (	2 S 2 L	30 30	C 27		24		C 20	18 19	16 17	15	13	c 11 12		ωα	7 (	თ ౮			ا ده د
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heat.  n aestivum  n aestivum  ta; Viridiplant  ta; Viridiplant  phyta; Magnol:  phyta; Magnol:  p; Triticeae; '1  p; Triticeae; '1  p; Tro 2125)  N.P. and Peng.  control of pla  WO 9909174-A 1  WO 9909174-A 1  Location/Qual  1. 2125  /organism="T]	2125 from GI:99		800	800	800	800	800	800	800	800	800	399	51	į		2255	309 1890	369 211	230	511	436	332	416	453	1746 377	2709	1768	2125
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ntae; Streptophyt liophyta; Liliops Triticum. Triticum. 3,7 lant growth and c lant 25-FEB-1999; L (GB); PENG JINN alifiers	DNA ent WO9909174.	ALIGNMENTS	AF377636 AF377637	AF3//633 AF377634	AF377632	AF377630	AF377628 AF377629	AF377626 AF377627	AF377625	AF377623	AF377621 AF377622	AX005856	AX005896	AX005808	AB030956 AC087797	AX005806	AX005855	AX005852 AX005851	AX005861	AX005854	AX005867 AX005863	AX005849	AX005809	AX005857	AX005848 AX005862	AX005794	TAE242531	25
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ATGAAGCGGGAGTACCAGGACGCCGGAGGGAGCGGCGGCGGCGGCGGCGGCATGGGCTCG
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Submitted (25-MAY-1999) Richards D.J
Innes Centre, Colney Lane, NR4 7UJ,
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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YFGEALARRVFRFPOPDSSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEAFAG
CRRVHVVDFGIKGMQMPALLQALALRFGGPPSFRLTTGGYGPPOPDSTDALQQVGWKLA
QFAHTIRVDFGIKGMQMPALLQALALRFGGPPSFRLTTGGYBPOPDSTDALQQVGWKLA
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QFAHTIRVDFQYRGLVAATLADLEFPHLQPBGEBDPNEPPEVLAVNSVEBHRLLADA
GFAHTIRVDFQYRGLVAATLADLEFPHLQPBGEBDPNEPPEVLAVNSVEBHRLLADG
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SM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embry
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Spermatophyta; Magnoliophyta; Liliopsida; Poi
Pooldeae; Triticaea; Triticum.

ICE 1 (bases 1 to 1768)

DRS Harberd, N.P. and Peng, J.

SRS Harberd, N.P. and Peng, J.

E Genetic control of plant growth and develop
(NAL Patent: WO 9909174-A 13 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (CORES

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Pooideae; Triticeae; Triticum.

1 (Dases 1 to 2709)
1 (Dases 1 to 2709)
1 Harberd, N.P. and Peng, J.
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Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticeae; Triticum.

1 (bases 1 to 1746)

Harberd, N. P. and Peng, J.

Genetic control of plant growth and development

Patent: WO 9909174-A 57 25-FEB-1999;

HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)

Location/Qualifiers
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Sequence 71
AX005862
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Harberd,N.P. and Peng,J.
Genetic control of plant growth and development Patent: WO 9909174-A 71 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Pooideae; Triticeae; Triticum.
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                                                  /organism="Triticum aestivum"
/db_xref="taxon:4565"
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Triticum aestivum
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                    Sequence 66 from Patent
AX005857
                                                                                   Genetic control of plant growth and development Patent: WO 9909174-A 66 25-FEB-1999; HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
                                                                                                                 Harberd, N.P. and Peng, J.
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                                             /organism="Triticum aestivum"
/db_xref="taxon:4565"
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1 (bases 1 to 416)

1 (bases 1 to 416)

Harberd, N. P. and Peng, J.

Genetic control of plant growth and development Patent: WO 9909174 A, 18 25-FEB-1999;

HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)

LOCALIO/Qualifiers
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Triticum aestivum
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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Harberd, N.P. and Peng, J.
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/db_xref="taxon:4565"
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Best Local Similarity
Matches 159; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                         AX005867 324 bp
Sequence 76 from Patent
AX005867
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AX005849
Triticum aestivum
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Harberd,N.P. and Peng,J.
Genetic control of plant growth and development
Patent: WO 9909174-A 58 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
               bread wheat
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/db_xref="taxon:4565"
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vagnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
AX005863
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1 (bases 1 to 324)
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1 (bases 1 to 436)
Harberd, N.P. and Peng, J.
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/db_xref="taxon:4565"
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/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                               Sequence 63
AX005854
AX005854.1
                                                                                                                                                                                                                    Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
                                                                                                                                             1 (bases 1 to 511)
Harberd,N.P. and Peng,J.
Genetic control of plant growth and development
Patent: WO 9909174-A 63 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
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/note="n is any nucleotide"
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                                                                                                        /organism="Triticum aestivum"
/db_xref="taxon:4565"
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Best Local Similarity 100.0%; Pred. No. 2.3e-45;
Matches 122; Conservative 0; Mismatches 0;
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Triticum aestivum

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticeae; Triticum.

1 (bases 1 to 357)

Harberd, N.P. and Peng, J.
                                                                                                                                                                                                                                                                                                                            AX005853 357 bp
Sequence 62 from Patent
AX005853
                                                                                                                                                                              Genetic control of plant growth and development
Patent: WO 9909174-A 62 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); FENG JINRONG (GB)
Location/Qualifiers
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/db_xref="taxon:4565"
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94; Conserv
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Triticum aestivum
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Sequence 70 from Patent
AX005861
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Location/Qualifiers
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Harberd, N.P. and Peng, J.
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/db_xref="taxon:4565"
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100.0%; Pred. No. 2.1e-38;
tive 0; Mismatches 0;
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Search completed: January 23, 2002, 04:54:37 Job time: 8226 sec	114 GACAGCTTCGCCACCCACCTCGCCACGGACACCG 147	265 gacagettegeeacetegeeaceggacaeeg 298	54 CTGGAGCAGCTCGAGATGGCCATGGGGATGGGCGCGTGGGCGCCGCCCCCCGAC 113	205 ctggagcagctcgagatggccatggggatgggcgtgggcggccggc

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                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                   2125
         659
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PT Prov
New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                Triticum aestivum.
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                                                P-PSDB; AAY02540.
                                                                                                    (PLAN-) PLANT BIOSCIENCE LTD
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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesi

biosynthesis;

Wheat Rht clone 5al genomic sequence.

16-JUL-1999 (first entry)

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Asstivum, inhibit growth of the plant. This growth inhibition is antagonised by glibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutraz e.g. to allow use of a gibberellin biosynthesis inhibitor to keep wee
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polynucleotides
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C The specification describes polypephinologues that, when expressed in Triticum Aestivum, innecessity its homologues) that, when expressed in Triticum Aestivum, innecessity its homologues) that, when expressed in Triticum Aestivum, innecessity its homologues that, which is growth inhibition is antagonised by growth of the products can be used to provide Rht mutant plants which are dwarfed compared with the product of the produce Rht mutant plants which are dwarfed compared with the compared by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds the composite DNA sequence of wheat Rht gene.
    provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
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Conservative

31.0%;

Score 659; DB 20; Pred. No. 4.2e-274; Mismatches

Length Indels

2709;

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Best Local Similarity
Matches 659; Conserv 1246 1190 1250 1130 1370 1310 1186 1126 1066 1006 1070 1010 946 886 950 826 890 766 706 770 646 ctcgtcgccgccacgctcgcggacctggagccgttcatgctgcagccggagggcgagga 1304 gtgggctggaagctcgcccagttcgcgcacacccatccgcgtcgacttccagtaccgcggc gccatcctggaggcgttcgccggctgccgcgtgcacgtcgtcgacttcggcatcaag cacgcgcacttctacgagtcctgcccctacctcaagttcgcgcacttcaccgccaaccag caggagaacctctccgccgcggaggcgctggtgaagcagatacccttgctggccgcgtcc acgcaggaggccgggattcggctggtgcacgcgctgctggcgtgcgcggaggccgtgcag acgcaggaggccgggattcggctggtgcacgcgctgctgctggcgtgcgcggaggccgtgcag gccccgccggtcgcggccggccaacgcgacgcccgcgctgccggtcgtcgtcgtcgac gccccgccggtcgcggccgcggccaacgcgacgcccgcgctgccggtcgtcgtggtcgac gtgggctggaagctcgcccagttcgcgcacaccatccgcgtcgacttccagtaccgcggc tcgttccgcctcaccggcgtcggccccccgcagccggacgagaccgacgcgccgcgcag ttccgcttccgcccgcagccggacagctccctcctcgacgccgccttcgccgacctcctc ctcgtcgccgccacgctcgcggacctggagccgttcatgctgcagccggagggggagga tcgttccgcctcaccggcgtcggcccccccgcagccggacgagaccgacgccctgcagcag cacgcgcacttctacgagtcctgcccctacctcaagttcgcgcacttcaccgccaaccag ttccgcttccgcccgcagccggacagctccctcctcgacgccgccttcgccgacctcctc cagggcggcgatgcgcaaggtcgccgcctacttcggcgaggccctcgccgcgcgtc caggagaacctctccgccgcggaggcgctggtgaagcagatacccttgctggccgcgtcc 0; 0; Gaps 1369 1245 1309 1249 1125 1065 1129 1005 1069 1009 1189 885 829 945 949 825 688 765

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                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 652; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                    Sequence 1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antagonist; gibberellin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rht gene; homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus cDNA sequence of wheat Rht clone C15-1.
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                                                                                                                                                                                                             653
                                                                                                                                                 713
                                                          127
187
                                                                                                                   67
                                                                                                                                 aggccgggattcggctggtgcacgcgctgctggcggtgcgcggaggccgtgcagcaggaga
                                                                                                                                                                                          cggtcgcggccgcggccaacgcgacgcccgcgctgccggtcgtcgtggtcgacacgcagg 712
            acctctccgcgggggggctggtgaagcagatacccttgctggccgcgctcccagggcg
                                                                                                                aggccgggattcggctggtgcacgcgctgctggcgtgcgcggaggccgtgcagcaggaga
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                                                       acctctccgccgcggaggcgctggtgaagcagatacccttgctggccgcgtcccagggcg
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                    BP;
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100.0%; Pr
0;
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                                                                                                                                                                                                                                                                                                                  A;
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                                                                                                                                                                                                                                                      DB 20; 1
4.5e-271;
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants
                                                                                                                                                                                                                                                                                                                New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
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paclobutrazol;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richards
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RESULT AAX36263 ID AAX3 AC AAX3 AC AAX3 AC DNA XX Rht KW Anta KW Pacl XX WO95 XX WO95 XX WO95 YN WO95 
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                                                                                                                New Triticum Aestivum polynucleotides - encoprovides inhibition of the growth of plants, antagonised by gibberellin, used to confer a
                                                                    Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                paclobutrazol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rht gene; homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence obtained after sequencing wheat Rht clone 14a1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX36263
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                                                                                                                                                                                                                   WPI; 1999-181040/15
                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum
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ilarity 100.0%;
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                                                                                                                                                                                                                                                               Peng J,
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                                                                                                                                                                                                                                                                                                                BIOSCIENCE LTD
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                                                                                                                                                                                                                                                                                                                                                                                                           98WO-GB02383
                                                                       2b(9);
describes polypeptides hat, when expressed in [
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum; wheat; growth inhibition; lin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                 Richards
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RESULT
AAX36283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; ss.
                                  Harberd
                                                                                                                                                                                                          07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                              Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Partial sequence of the wheat rht-10 allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX36283 standard; DNA; 416
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                                                                                          (PLAN-) PLANT BIOSCIENCE LTD
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Pred. No. 1.6e-98;
D; Mismatches 1
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Best Local Similarity
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                                                                                                                                                                                                                 Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes polypeptides encoded by the Rht gene (a its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by globberellin. The products can be used to provide Rht expression in plants of the products can be used to provide Rht expression in the products.
                                                                                                                                                                    Triticum aestivum
                                                                                                                                                                                                     paclobutrazol; ss.
                                                                                                                                                                                                                                                                  DNA sequence obtained after sequencing wheat Rht clone 5al.
                                                                                                                                                                                                                                                                                                         16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                         AAX36270 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 12a; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                 13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 416 BP; 59 A; 168 C; 129 G; 60 T; 0 other;
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 (PLAN-) PLANT BIOSCIENCE LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agctcaacgcctccacctcctccaccgtcacgggcagcgggctacttcgatctcccgc 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gcgggagcagcacctcgtcgtcatcctcctcctcgtc 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgacggcgccggcctgtccgccgactccgtgcgggatcccaagcggatgcgcactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agotoaacgcotocacctcctccaccgtcacgggcagcggctacttcgatctcccgc 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                       (first entry)
                                 97GB-0017192.
                                                                98WO-GB02383
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Best Local Similarity
Matches 260; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1865 tcgccacctcggcatggcgctggccgtggtatctcgcgagtttttgaacgctgtaag 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 5al.
                                                                   Triticum aestivum
                                                                                                                   Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with used to produce Rht mutant plants which are dwarfed compared with
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                                                                                                                                                                                                                16-JUL-1999
                                                                                                                                                                                                                                                                                     AAX36255 standard; DNA; 332
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                                                                                                                                                                                                                                                                                                                                                                            252
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                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                           gtggatggacgacgaactccg 2125
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                                                                                                                                                                                                                                                                                                                                                                           gtggatggacgacgaactccg
                                                                                                                                                                                                                                                                                                                                                                                                                                               tacacatcgtgagcatggaggacaacacagccccggcggccgcccccggctctccggcgaa
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                                                                                                                                                                             obtained
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                                                                                                                                                                         after sequencing wheat Rht clone 14a1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 210; DB 20;
Pred. No. 6.9e-81;
0; Mismatches 1;
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RESULT 10
AAX36273;
ID AAX36273;
XX
AC AAX36273;
XZ
DT 16-JUL-1999 (first entry)
XX
DE DNA sequence obtained after seque
XX
DE NA sequence obtained after seque
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DE NA sequence obtained after seque
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DE DNA sequence obtained after sequence
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DE DNA sequence obtained after sequence
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Best Local
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                                                                                                                                                                                                                                                                                               antagonist; gibberellin; dwarf phenotype;
                                                                                                                                                                                                                                                                                                                               Rht gene; homologue; Triticum aestivum; wheat;
                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence obtained after sequencing wheat Rht clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cctcgttccgcctcaccggcgtcggccccccgcagccgg 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agcaggggatgcagtggcccgcacttctccaggccctcggccctccgtcccggcggccctc 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cctcgttccgcctcaccggcgtcggccccccgcagccgg
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Conservative (
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                                                                                                                                                                                                                                                                                           heat; growth inhibition; gibberellin biosynthesis;
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RRESULT 1
AAX3629
ID AAX37
XX AAX3
AC AAX3
XX DE DNA
XX Rht
KW Rht
KW Pacl
XX Trit
XX W099
PN W099
PN W099
PN 25-F
XX PF 07-A
XX N 13-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                     25-FEB-1999
                                                                                                      W09909174-A1
                                                                                                                                          Triticum aestivum
                                                                                                                                                                            paclobutrazol;
                                                                                                                                                                                        Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                              DNA sequence
                                                                                                                                                                                                                                                                                16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                    AAX36269 standard; DNA; 436 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 324 BP;
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                                                                                                                                                                                                                                              obtained
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                                                                                                                                                                                                                                            after sequencing wheat Rht clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 157; DB
; Pred. No. 4.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 20;
. 4.4e-58;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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07-AUG-1998;

98WO-GB02383

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RESULT 12
AAX36260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 5al.
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                                                                                                                                                                                             Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                        W09909174-A1
                                                                                                                                                     Triticum aestivum
                                                                                                                                                                                   paclobutrazol; ss.
                                                                                                                                                                                                                                           DNA sequence obtained after sequencing wheat Rht clone 14al.
                                                                                                                                                                                                                                                                              16-JUL-1999
                                                                                                                                                                                                                                                                                                                                       AAX36260 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 436 BP; 58 A; 153 C; 141 G; 66 T; 18 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2c(2); 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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(PLAN-) PLANT BIOSCIENCE LTD
                              13-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                   196
                                                                                                                                                                                                                                                                                                                                                                                                                                574 agcagcacctcgtcgtcatcctcctc 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agcagcacctcgtcgtcatcctcctc 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.9%; Score 146; DB 20; ilarity 100.0%; Pred. No. 2.3e-53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peng J,
                              97GB-0017192.
                                                            98WO-GB02383.
                                                                                                                                                                                                                                                                                                                                        DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195
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ARESULT 1
AAX36259
ID AAX3
XX AAX3
AC AAX3
DT 16-J
XX DNA
XX DNA
XX ANT
KW ANT
KW ANT
KW Pacll
XX Trit
XX W099
PN W099
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 14al.
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                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX36259 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 511 BP; 125 A; 137 C; 117 G; 119 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2b(6); 88pp; English.
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   Harberd NP,
                                                                                                                                                                                        07-AUG-1998;
                                                                                                                                                                                                                                                                                                                   W09909174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence obtained after sequencing wheat Rht clone 14a1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harberd NP,
                                                              (PLAN-) PLANT BIOSCIENCE LTD
                                                                                                                             13-AUG-1997;
                                                                                                                                                                                                                                                       25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                paclobutrazol; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 tg 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcctggccgggccgtgatctcgcgagttttgaacgctgtaagtacacatcgtgagcatgg 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Peng J,
                                                                                                                             97GB-0017192
                                                                                                                                                                                        98WO-GB02383
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   Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT: 14
AAX362
XX AAX362
XX AAX362
XX I 16-JUL
XX Rht ge
KW Rht ge
KW Paclob
XX Tritic
XX WO9909
PN WO9909
PN WO9909
PN 25-FEB
XX O7-AUG
XX O7-AUG
PF 13-AUG
XX (PLAN-
XX Harber
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XX WPI; 1
XX New Tr
PT Provid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 14a1.
New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                      Rht gene; homologue; Triticum aestivum; wheat; antagonist; gibberellin; dwarf phenotype; gibby paclobutrazol; ss.
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                                                                              WPI; 1999-181040/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                           (PLAN-) PLANT BIOSCIENCE LTD
                                                                                                                                                                                               13-AUG-1997;
                                                                                                                                                                                                                                    07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence obtained after sequencing wheat Rht clone 14a1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-1999 (first entry)
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                                                                                                                  Peng J,
                                                                                                                                                                                               97GB-0017192
                                                                                                                                                                                                                                    98WO-GB02383
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                                                                                                                      Richards
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                                                                                                                                                                                                                                                                                                                                                                                                      heat; growth inhibition; gibberellin biosynthesis;
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                       which
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AAX36258
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Best Local
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                                                                                        New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum.
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                                                                                                                                                                                                                      (PLAN-) PLANT BIOSCIENCE
                                                                                                                                                                                                                                                     13-AUG-1997;
                                                                                                                                                                                                                                                                                    07-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                paclobutrazol; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence obtained after sequencing wheat Rht clone 14a1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2b(13); 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 ctggagcagctcgagatggccatggggatgggcggtgggcgcggcgcggcccccgac 264
                                                                                                                                                        1999-181040/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                       Peng J,
                                                                                                                                                                                                                                                      97GB-0017192
                                                                                                                                                                                                                                                                                    98WO-GB02383
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100.0%; Pred. No.
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by

Disclosure; Fig 2b(4); 88pp; English.

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                                                                                                                                                                                                                           1096 gccctcgccctccgtcccggcggccctccctcgttccgcctcaccggcgtcggccccccg 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 14al.
                                                                                              1156 cagccggacgacgacgccctgcagcaggtgggctggaagctcgcccagttcgcgcac 1215
Sequence 369 BP; 55 A; 142 C; 105 G; 53 T; 14 other;
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AU095344 AU09534 R
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BG051785 FM1\_8\_D0
BF655617 FM1\_46\_D1
AU222715 AU222715
AU065169 AU065169 AU065169
BG411689 EM1\_60\_F1
AL57799 UI-R-AB0-AL506960
AL881894 606074G08
AL18677799 UI-R-AB0-AL506960
AL881894 606074G08
AL967572 Lj1rnpest
AV407563 AV407563
AV407163 AV407142
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Copyright (c) 1993 - 2000 Comp
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BG308975 HVSMEC000
A1770444 606052F10
BF268018 HV_CE001
BF268018 HV_CE001
BF618807 HVSMEC000
BE364489 PI1_14_F0
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BE414891
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DEFINITION
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AUTHORS
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                               source
                                         Unpublished (2000)
Contact: Warburton M
Applied Biotechnology Center, CIMMYT
Apdo. Postal 6-641, 06600 Mexico DF MEXICO
Tel: 52-5-72679091 ext 1381
Fax: 52-5-726758/59
Email: mwarburton@cgnet.com
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                             1 (bases 1 to 400)

Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvara),G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.

International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                           Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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/organism="Triticum aestivum"
/cultivar="Atlas"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Triticeae, Triticum.

1 (bases 1 to 268)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.

The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oandersn@pw.usda.gov
ce have been trimmed to remove vector
                   and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside, Plasmid DNA
                                                                                                                                       /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in t greenhouse. Whole spike with awns trimmed, white,
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/tissue_type="root"
/dev_stage="8 day old"
/note="Vector: pYES2 (Invitrogen); 0.5-1.5 Kbp average
insert_size."
preparations and DNA sequencing were performed
                                                                                                                                                                                                                                   /clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4565"
/clone="dummon"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U.
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Seq primer: AATTAACCCTCACTAAAGGG
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HVcDNA0003 (Etiolated and unstressed)"
/tlssue_type="Seedling shoot"
/lab_host-"TJC121"
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100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
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Seq primer: AATTAACCCTCACTAAAGGG
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HV_CE30019J17f Hordeum vulgare seedling green leaf EST library
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HV_CE30019J17f, mRNA sequence.
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              Unpublished (2000) on Nov 17, 2000 this sequence version replaced \mathfrak{gl}:11199013
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
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Tel: 650 723 2227
Fax: 650 725 8221
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/lab_host="xLOLR (Stratagene)"
/note="Organ: immature ear; Vect;
Site_2: XhoI; Mixed ear tissue
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Maize ESTs from various cDNA libraries sequenced
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/db_xref="taxon:4577"
/clone_lib="606 - Ear tissue cDNA library from Schmidt
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                                                                                                                                              Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Hordeum.
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Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 587.
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Unpublished (2000)
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/Cultivar="CI16155 (MIAI3)"
/db_xref="faxon:4513"
/clone="HV_CEA0019J17f"
/clone="HV_CEA0019J17f"
/clone_lib="Hordeum vulgare seedling green leaf EST library HVCDNA0004 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/tissue_type="seedling green leaf"
/tissue_type="seedling green leaf"
/tissue_type="seedling green leaf"
                                       /organism="Hordeum vulgare"
/cultivar="Morex"
clone="HVSMEc0007P09f"
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Sequences have been tr
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HVcDNA0003 (Etiolated and unstressed)"
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/db_xref="taxon:4558"
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/lab_host="TJC121"
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45; Conser
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Tel: 650 723 2227
Fax: 650 725 8221
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Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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949053 row: G col
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                                                                                                                       Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing. 8 others
                                                                                                                                                                                                                                                          /note-"Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda
                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="immature leaf primordium and vegetative meristem" \,
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/cultivar="W64A"
/db_xref="taxon:4577"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
                                                                                                                                                                                                                                                                                                                                         /dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE595338 527 bp mRNA EST 18-AUG-2000 PI1_48_G12.b1_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
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Unpublished (2000)
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1 (bases 1 to 527)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mmpratt@uga.edu
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=Torgan: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
cultivar) were infected with pathogen (isolate FRM42I of
Collectorrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
                                                                                                                                                                                                                                                                                                                                                                                                                                               sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host
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/note="Organ: Anthracnose-infected le
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/db_xref="taxon:4558"
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BG713881
                                                              Sorghum bloolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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 Unpublished (2000)
            1 (bases 1 to 592)
Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.
An EST database from Sorghum: developing embryos
                                                                                                                                                      EST
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EM1_60_F10.g2_A002
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Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The University of Georgia Plant Sciences Building,
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1 (bases 1 to 563)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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/note="Organ: Floral-induced meristems; Vect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Sorghum propinquum"
/db_xref="taxon:132711"
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BASE COUNT
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Contact: Cordonnier-Pratt
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 658)
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Department of Botany
The University of Georgia
Plant Sciences Building, Rm.
                                                                                                                                                                                                                                                   The University of Georgia Plant Sciences Building, 1 Tel: 706 542 1860 Fax: 706 542 1805
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BF587541
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Sequences have been tr
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High quality sequence stop: 583
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                                                                                                                                              Seq primer: PolyTMix
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                                                            Location/Qualifiers
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/db_xref="taxon:4558"
/clone_lib="Embryoo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
/organism="Sorghum propinquum"
/db_xref="taxon:132711"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Friticeae; Hordeum.
1 (bases 1 to 977)
1 (bases 1 to 977)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Young,R., Close,T.J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE196286 977 bp mRNA EST
HVSMEh0091004f Hordeum vulgare 5-45 DAP spike
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for barley genomics
Unpublished (2000)
On Jun 26, 2000 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE196286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact:
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                                                                                                                                                                                                                                                                                                                                                                              il: rwing@clemson.edu
primer: AATTAACCCTCACTAAAGGG
h quality sequence stop: 618.
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              /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 272 c 270 g 197 t 4 others
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Email: rwing@clemson.edu
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OR-938-291A-8/c  908-938-291A-8/c  908-938-291A-8/c  908-938-291A-8/c  908-938-291A-8/c  908-938-291A-8/c  908-938-291A-8/c  808-938-291A-8/c  808-938-291A-8/c  808-938-291A-8/c  808-938-291A-8/c  808-938-291A-8/c  808-938-291A-8/c  808-938-291A-8	19 0.9 472 3 US-09-249-471-3 19 0.9 472 3 US-09-249-472-3 19 0.9 472 3 US-09-249-451-3 19 0.9 472 3 US-08-809-459-361-3 19 0.9 472 3 US-08-249-461-3 19 0.9 477 2 US-08-465-380-3 19 0.9 477 2 US-08-466-399-3 19 0.9 477 2 US-08-461-399-3 19 0.9 477 3 US-08-249-461-3 19 0.9 477 3 US-09-249-451-3 19 0.9 477 3 US-09-249-461-3 19 0.9 477 3 US-09-249-461-3 19 0.9 477 3 US-09-249-461-3 19 0.9 3358 2 US-08-469-537A-
TED	3 Sequence 33, Appl 3 Sequence 33, Appl 3 Sequence 33, Appl 3 Sequence 33, Appl 5 Sequence 33, Appl 5 Sequence 35, Appl 5 Sequence 35, Appl 5 Sequence 35, Appl 6 Sequence 35, Appl 7 Sequence 35, Appl 8 Sequence 35, Appl 8 Sequence 35, Appl 9 Sequence 35, Appl

Query Match

1.0%;

Score

22; DB 3;

Length 4308;

Best Local Similarity 100.0%; Matches 22; Conservative

0;

Pred. No. 1.5;

Mismatches

0;

Indels

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Gaps

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; TOPOLOGY: 1:; MOLECULE TYPE: US-09-082-092-9
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                Query Match 1.0%; Score 21; DB 4; Best Local Similarity 100.0%; Pred. No. 4.3;
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,221
FILING DATE: 20-MAY-1997
APPLICATION NUMBER: 60/060,465
FILING DATE: 30-SEP-1997
APPLICATION NUMBER: 60/075,940
FILING DATE: 25-FEB-1998
APPLICATION NUMBER: 60/077,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/082,092
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                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/077,033
FILING DATE: 06-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
BREFERENCE/DOVET NUMBER: 10461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield &
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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TITLE OF INVENTION:
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CLASSIFICATION:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                         TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: L0461/7032
                                                                                                                                                                                    LENGTH:
   21;
                                                                                                                                                             nucleic acid
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                                                                                                                                                                              1491 base pairs
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Landstrom, Marene
Heldin, Nils-Erik
Heldin, Carl-Henrik
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 Conservative
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TENTION: SMAD7 AND USES THEREOF
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Moren, Anita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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 Mismatches
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                                 Length 1491;
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RESULT 4
US-08-118-200-1
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; MOLECULE TYPE:
US-08-314-309A-10
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US-08-314-309A-10/c
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                                                           Sequence 1, Application US/08118200 Patent No. 6197500
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                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                Query Match
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TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1
                                              GENERAL INFORMATION:
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                APPLICANT: APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 590 base pairs
TYPE: nucleic acid
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PROCESS FOR PRODUCING 7-AMINOCEPHEM TITLE OF INVENTION: COMPOUND OR SALTS THEREOF NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FUKAGAWA, MASAO APPLICANT: IWAMI, MORITA
APPLICANT:
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                                                                                                                                                          153
                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 30-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
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                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IWAMI, MORITA
ARAMORI, ICHIRO
 SCHLESSINGER, David
                SUTHERLAND, Grant R RICHARDS, Robert I
                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                            unknown
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                                                               Sequence 1, Application US/08458745 Patent No. 6242576
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                                  GENERAL INFORMATION:
APPLICANT: SUTHER
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,200
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 23-DEC-1992
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APPLICATION NUMBER: US 07/802,650
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,232
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA SEQUENCES RELATED TO ISOLATED ITLE OF INVENTION: FRAGILE X SYNDROME
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                   APPLICANT:
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                                                                                                                                                                          59 gcggcggcggcggtggcggc 78
                                                                                                                                                                                                                         Local Similarity 100.
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 04-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                             GCGGCGGCGGCGGC 415
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22313-1404
                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                     1028 base pairs
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MANDEL, Jean-Louis
PRITCHARD, Melanie April
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KREMER, Eric J
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RICHARDS, Robert I
SCHLESSINGER, David
                                                                                                                                                                                                                                                                                                                                                                                                                                       (703) 836-2021
                                 SUTHERLAND, Grant
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В
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                                             Query Match
Best Local Similarity 100.
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APPLICATION NUMBER: US 08/118,200
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: US 07/802,650
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,232
FILING DATE: 20-MAR-1991
                                                                                                                                                                                                                                                TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION NUMBER: US 07/966,517
PRILING DATE: 23-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 04-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/458,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                59 gcggcggcggcggtggcggc 78
                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                               TELEPHONE:
GCGGCGGCGGCGGC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22313-1404
                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                            Crane-Feury, Sharon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYNCH, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MULLEY, John C
MANDEL, Jean-Louis
PRITCHARD, Melanie April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , UY
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KREMER, Eric J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAKER, Elizabeth
                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US 07/638,518
04-JAN-1991
                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1995
                                                                                                                                                                                   single
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                                                                        0.9%;
                                                                                                                                                                                                                                                                                                               020160-164
                                                          0;
                                                                        Score 20;
Pred. No.
                                                             Mismatches
                                                                          DB 4;
12;
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                                                                                       Length 1028;
                                                             Indels
                                                           0;
                                                           Gaps
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US-08-403-634-1/c

Sequence 1, Application US/08403634
Patent No. 5674748

APPLICANT:

Giordano,

Antonio

RESULT

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RESULT 7
US-08-913-441B-1/c
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                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: No. 6162612el Human Cyclin
TITLE OF INVENTION: Methods of Using The Same
FILE REFERENCE: 8321-76 CI1
                                           SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08913441B Patent No. 6162612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                            FILE REFERENCE: 8321-76 CI1
CURRENT APPLICATION NUMBER: US/08/913,441B
CURRENT FILING DATE: 1997-12-02
PRIOR APPLICATION NUMBER: 08/403,634
PRIOR FILING DATE: 1995-03-14
PRIOR APPLICATION NUMBER: PCT/US96/03557
PRIOR FILING DATE: 1996-03-14
                                                         NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVI
TYPE: DNA
                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1482
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,575
FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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LENGTH: 1461 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 caacgcgccgccgccgcccc 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                             55 CAACGCGCCGCCGCCGCCCC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 0.9%; Score 20; Local Similarity 100.0%; Pred. No. les 20; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz ADDRESSEE: No. 5674748ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                      1461
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                                                                                                                                                                                                                                                         6162612el Human Cyclin-Dependent Kinase-Like Proteins and
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; LOCATION: (65)..(1180)
US-08-913-441B-1
US-08-923-454A-17
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Best Local Similarity
                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
                                                       MOLECULE TYPE:
HYPOTHETICAL: |
ANTI-SENSE: NO
                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                            FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
                                        FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 709 Swederand CITY: King of Prussia
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                                                                                                                                                                                                        TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                              2036 base pairs
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Livi, George
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Clinkenbeard,
                                                          Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                      CDNA
            Feature polymorphism at 1325
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100.0%; Pred. No
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Query Match Best Local Similarity

0.9%;

Score 20; Pred. No.

DB 11;

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Length 2036;

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RESULT 10
US-08-314-309A-1/c
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                                                                                                                                                                                                                                                                                       ; LOCATION: 1..2205
; OTHER INFORMATION: /note= "mutTM1-TM2"
US-08-888-077A-41
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                          Sequence 1, Application US/08314309A Patent No. 5677141
GENERAL INFORMATION:
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 41, Applicat Patent No. 6020143
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/888,077A FILING DATE: 03-JUL-1997 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541 FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (908) 654-7866
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: PALISI, THOMAS M
REGISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-5000
                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2205 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                             113 GCGGCGGCGGCGGTGGCGGC 94
                                                                                                                                                              59 gcggcggcggcggtggcggc 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2205 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: WESTFIELD
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                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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                                                                                                                                                                                                           20;
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FUKAGAWA, MASAO
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                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                     Sequence 20, Patent No. 5
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                                                              STATE:
                                                                                              STREET:
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; TOPOLOGY: ur
; MOLECULE TYPE:
US-08-314-309A-1
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Best Local Similarity
Watches 20; Conserve
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TELEPAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Oblon, No. 5677141man
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,309A
FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                     TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED TITLE OF INVENTION: SECRETORY ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                        APPLICANT: Ma, Julian K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                 123 ggagggggaggaggtggacg 142
                                                                                                                                                                                                                                                                                                                                                                            484 GGAGGGGGAGGAGGTGGACG 465
                                 COUNTRY: UZIP: 92037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H: 3172 base pairs nucleic acid
                                                                                                                                                                                                                                                                        0, Application US/08642406A
5959177
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                                                                                   La Jolla
                                                                 California
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                                                                                                   E: THE SCRIPPS RESEARCH INSTITUTE 10666 No. 5959177th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1755 S.
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                                                                                                                                                                                                                     Hein, Mich B.
Hiatt, Andrew C.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Floppy disk
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21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5677141man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROCESS FOR PRODUCING 7-AMINOCEPHEM COMPOUND OR SALTS THEREOF
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SOFTWARE: Patentin Rel

PatentIn Release #1.0, Version #1.25

OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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US-08-434-000A-1/c
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                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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LENGTH: 3517 base pairs
TYPE: nucleic acid
                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHBER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/427,765 FILING DATE: 27-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/591,823 FILING DATE: 02-OCT-1990 PRIOR APPLICATION DATA:
                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                       OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
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CLASSIFICATION:
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   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
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: including application
: described below:
08/367,395
                                                                                                      US/08/434,000A
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00.0%; Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 552-0159
TELEX: 67-3510
TELEX: SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3517 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09312157 Patent No. 6303341 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.9%;
Best Local Similarity 100.0%;
SEQUENCE LISTING INFORMATION FOR SEQ ID NO: 1:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
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                                                                               REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 552-8400
                                                                                                                                     FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90071
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
VENTUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
                                                           TELEFAX: (619) 552-0159
                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/312,157 FILING DATE: 14-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
                                          TELEX: 67-351
                                                                                                                                                                                                            APPLICATION NUMBER: 08/434,000
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Pred. No
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NAME/KEY: Coding Sequence;
LOCATION: 124...2445;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-312-157-1
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Session 
                                                                           Query Match 0.9%; Sometive 0.9%; Sometimes 20; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
CLASSIFICATION: MAY 10, 1994
CLASSIFICATION: NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REGISTRATION NUMBER: 29,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Live
CITY: Washington
STATE: D.C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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APPLICANT: Ambrose, Christine M.
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                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9997 base pairs TYPE: nucleic acid STRANDEDNESS: both
59 gcggcggcggcggtggcggc 78
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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90..9446
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                                                                                                                      Score 20;
Pred. No.
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9.5;
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Search completed: January 23, 2002, 05:00:59 Job time: 5192 sec
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REPERENCE/DOCKET NUMBER: 0609.3880003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Patent No. 5
                                                                                                                                               Matches
                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 9997 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Guyao, Madel F.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                 195 GCGGCGGCGGCGGCGC 176
                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
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                                                                                                  59 gcggcggcggcggtggcggc 78
                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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5693757
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Ambrose, Christine M.
                                                                                                                                                Conservative
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90..9446
                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                               371-2540
                                                                                                                                                              0.9%;
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                                                                                                                                                              Score 20;
; Pred. No.
                                                                                                                                                0
                                                                                                                                                Mismatches
                                                                                                                                                                DB 1;
9.5;
                                                                                                                                                0;
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0;

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Title:
Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Word size :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_1101:*
\:\/SIDS8/gcgdata
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SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:

*/SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:

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*/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:

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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gcgdata/geneseq/geneseqp/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

11	10	9	8	7	6	s	4	ω	N	Ľ	Result No.
80	8	80	8	9	9	9	9	9	9	13	Score
61.5	61.5	61.5	61.5	69.2	69.2	69.2	69.2	69.2	69.2	100.0	Query
234	195	188	183	282	282	223	216	182	33	623	Query Match Length DB
21	21	21	21	22	22	18	22	22	21	20	BG
AAB32786	AAG07313	AAG07314	AAG07315	AAB80896	AAB95859	AAW21733	AAB80892	AAB80893	AAG27119	AAY02540	ID
Eucalyptus grandis	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Human ATFx with N-	Human protein sequ	NIP-1 encoded by c	Human ATFx. Homo	Human ATFx leucine	Zea mays protein f	Protein encoded by	Description

4 # 51 #	- 4-	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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22	) ) )	22	22	22	22	20	20	19	19	18	18	22	22	22	21	20	21	20	17	18	20	18	18	17	17	17	22	22	22	22	22	22
AAB95652	AAM03303	AAM30551	AAM28043	AAM18038	AAM15554	AAY38971	AAY39108	AAW64306	AAW81669	AAW32366	AAW32434	AAM04489	AAM29259	AAM16772	AAG02396	AAY04937	AAB12072	AAY41643	AAW05473	AAW38923	AAY41635	AAW39015	AAW38959	AAW05491	AAW05419	AAW06861	AAM41059	AAM39273	AAB93086	AAG90541	AAB79242	AAB79117
e i	626.7# 9PJ	ide #458	#208	#	Peptide #1988 enco	r	M. tuberculosis an	Mycobacterium tube	M. tuberculosis im	Mycobacterium tube	Mycobacterium tube		Peptide #3296 enco	#3206 e		Mycobacterium spec	SH3 binding domain	Mammalian ion chan	SH3-binding peptid	Peptide resembling	20			Ω		Peptide binding th	Human polypeptide		_	gro	Corynebacterium gl	Corynebacterium gl

## ALIGNMENTS

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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; glbberellin biosynthesis;
                                                                                                                                                                                                                                                                                 Protein encoded by wheat Rht clone 5al genomic sequence.
                                                                                                                                                                                                                                                                                                       16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                               AAY02540;
                                                                                                                                                                                                                                                                                                                                                    AAY02540 standard; Protein; 623
New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                        13-AUG-1997;
                                                                                                                                              07-AUG-1998;
                                                                                                                                                                                         WO9909174-A1.
                                                                                                                                                                                                                Triticum aestivum.
                                                                                                                                                                                                                                      paclobutrazol.
                                           WPI; 1999-181040/15.
N-PSDB; AAX36279.
                                                                              Harberd NP,
                                                                                                   (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                                                                                                    25-FEB-1999.
                                                                          Peng J,
                                                                                                                         97GB-0017192.
                                                                                                                                              98WO-GB02383.
                                                                              Richards DE;
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RESULT

AAG27119

ID

AAG27119

AAG2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes polypeptides encoded by the Rht gene (and Cits homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by growth of the plant. This growth inhibition is antagonised by growth of the plant. This growth inhibition is antagonised by glaberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds charf but let crop plants grow tall. The present sequence is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 13
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

16-APR-1999

23-APR-1999

30-APR-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2000EP-0301439.
99US-0129845.
99US-0130077.
99US-0130449.
99US-0130510.
99US-0130891.
99US-0131449.
99US-0132407.
99US-0132484.
99US-0132484.
99US-0132486.
99US-0132487.
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990S-0123180

990S-0125788

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990S-0126264

990S-0126785

990S-0126785

990S-0128714
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21-MAY 1999
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11-JUN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
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14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
990S-0134221
990S-0134768
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990S-0135523
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99US-0145145. 99US-0145218. 99US-0145224. 99US-0145276. 99US-0145913.

99US-0147302. 99US-0147192. 99US-0147260. 99US-0147303.

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99US-0146389. 99US-0147038. 99US-0147204.

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Matches 9
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28-OCT-1999
29-OCT-1999
                                            The present invention relates to a method for identifying a modulator of gamma aminobutyric acid_B (GABA_B) receptor-mediated activity, by monitoring the interaction between a CREB/AFF transcription factor capable of binding to GABA_B receptor. The present sequence is the leucine zipper domain of human AFFx (see AAB80892), which was used in the method of the present invention. AFFx is a member of the CREB/AFF family of transcription factors. AFFx contains a bZIP domain, by which it interacts with the coiled coil domain of GABA_B receptor activity are useful for treating central nervous system or peripheral nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                                   Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor and the CREB/ATF transcription factors in the presence of a test
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                                                                                                                                                                                                                                                                                                                  Claim 14;
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N-PSDB; AAF77878.
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12-JAN-2000; 2000GB-0000516
  Sequence
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                                                                                                                                                                                                                                                                                                                  Page
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    182
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9905-0161361
9905-0161920
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9905-0161923
9905-0161923
  AA;
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Pred. No. 0.1
0; Mismatches
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29-AUG-1999
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990S-014733 990S-0147733 990S-0147733 990S-014831 990S-014831 990S-0149368 990S-0149368 990S-014972 990S-014972 990S-014972 990S-014972 990S-014972 990S-014993 990S-015086 990S-015086 990S-015106 990S-015106 990S-015133 990S-0152768 990S-0152768 990S-0152768 990S-0152768 990S-0152768 990S-0158779 990S-0158659 990S-0158659 990S-0158659 990S-0158659 990S-0158659 990S-0158659 990S-0158659 990S-0159786 990S-0159786 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0160768 990S-0160768 990S-0160768

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                                                                                                                                                                                                                                                                                                                                Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor and the CREB/ATF transcription factors in the presence of a test
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                                                                                                                                                       Sequence
                                                                                                                                                                            central nervous system or peripheral nervous system disorders.
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                                                                                                                                                                                                                                                                                               Claim 14; Fig 1; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-265904/27.
N-PSDB; AAF77877.
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12-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription factor.
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                                                                                                                                                       216 AA;
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2000GB-0000516.
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Best Local
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                                                                                                                                                                                                                                                                                                                                          The sequences given in AAW21733-35 represent NuMA binding proteins (NuMA = nuclear mitotic apparatus). These protein sequences were identified using the fusion proteins given in AAW21731-32. Compounds which interfere with the interaction of NuMA with a known NLP (NuMA interacting protein) are used to modulate cell division and/or proliferation. Ab, raised conventionally using NLP-1 or -2 as immunogen, are used to detect NLP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NLP which may be. markers for aberrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NuMA or NLP, it can be treated by administration of the appropriate functional protein. This protein is rich in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McPherson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIP-1 encoded by clone 59
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             Human; primer; detection; diagnosis; antisense therapy;
                                      Human protein sequence SEQ ID NO:18922.
                                                                 26-JUN-2001
                                                                                           AAB95859;
                                                                                                                    AAB95859 standard; Protein; 282
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                  proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 28; Page 57-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding nuclear mitotic appts. interacting proteins - useful for modulating cell division and prolifera
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    NIP-2; NuMA; nuclear mitotic apparatus; NuMA interacting protein;
division; proliferation; antibody; Ab; detection;
gnant cell growth.

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DB; AAT77784.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence, are the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence, are the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence, are the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence, are the oligonucleotide comprises at least 15 nucleotides and the combination of the sequence, are the oligonucleotide comprises at least 15 nucleotides and the combination of the sequence are the oligonucleotide comprises at least 15 nucleotides and the combination of the sequence, are the oligonucleotide comprises at least 15 nucleotides and the combination of the sequence are the oligonucleotide comprises at least 15 nucleotides and the combination of the sequence are the oligonucleotides are the sequence are the oligonucleotides and the combination of the sequence are the oligonucleotides are the sequence are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers sets can be used in antisense therapy and in gene therapy. The primers are slow useful for the particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB9593 represent human amino acid sequences; and AAH13629 to AAH13632 represent coligonucleotides, all of which are used in the exemplification of the present invention.
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09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
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                                                                       30-MAY-2001 (first entry)
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                          Human ATFx with N-terminal extension
                                                                                                                               AAB80896;
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2000JP-0118776.
2000JP-0183767.
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(, Otsuki T;
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termination

sequence

hybridisation assay; genetic

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter.

Arabidopsis thaliana protein fragment SEQ ID NO: 4422.

17-OCT-2000 AAG07315;

(first entry)

AAG07315 standard;

Protein; 183

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25-FEB-2000; 2000EP-0301439

06-SEP-2000

Arabidopsis thaliana

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Matches 9
                                                                                                                                  The present invention relates to a method for identifying a modulator of gamma aminobutyric acid_B (GABA_B) receptor-mediated activity, by monitoring the interaction between a CREB/ATF transcription factor capable of binding to GABA_B receptor. The present sequence is human ATFx, which was used in the method of the present invention. ATFx is a member of the CREB/ATF framily of transcription factors. ATFx contains a bZIP domain, by which it interacts with the coiled coil domain of GABA_B receptor. Modulators of GABA_B receptor activity are useful for treating central nervous system or peripheral nervous system disorders. The present sequence has an N-terminal extension compared to AAB80892.
                                                                                                                                                                                                                                                                                                                                            Identifying modulators of gamma aminobutyric acid(GABA)-B receptor mediated activity by monitoring the interaction between GABAB receptor and the CREB/ATF transcription factors in the presence of a test
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                                                                                                                                                                                                                                                                                                   Claim 14; Fig 9; 71pp;
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                                                                                                         Sequence
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12-JAN-2000; 2000GB-0000516
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  25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction hybridisation assay; genetic mapping; gene \varepsilon termination sequence.
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                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
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Similarity 100.0%;
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99US-0121825.
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The present invention relates to novel plant transcription Eucalyptus grandis or Pinus radiata. The present sequence i
                                                                                                    New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                             Wood M,
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18-AUG-1999;
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                                                   Claim 8; Page 304; 747pp; English
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|pppplppa 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP family of G-box binding factors, basic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements and MYB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium
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99DE-1032125
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100.0%; Pr/
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Pred. No.
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Best Local
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C. qlutami
                                                                                                                                                                                                                                                             carbohydrate; aromatic compound; vitamin; cofact diagnosis; Corynebacterium diphtheriae; genetic
                                                                                                                                                                                                                                                                                      fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis and adaptation (HA) proteins given in AAB79023 to AAB79242. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 399-400; 712pp; English
                                                                                                                                                                                                Corynebacterium
                                                                                                                                                                                                                                              Brevibacterium;
                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum; homeostasis; adaptation; HA protein; fine chemical production; organic acid; proteinogenic amino acid
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or enzymes -
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25-JUN-1999;
                                             23-JUN-2000; 2000WO-IB00911.
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les 8; Conserv
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99US-0141031
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                                                                                                                                                                                           glutamicum.
                                                                                                                                                                                                                                              environmental
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o. 5;
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09-JUL-1999;
09-JUL-1999;
                                                                                 AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis and adaptation (HA) proteins given in AAF7923 to AAF79242. The C. glutamicum HA genes (I) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polyketide or enzyme. The amino acids produced can be lysine, glutamine, glutamate, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, prodine, histidine, tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynebacterium alphtheriae. (I) can be used to map the C. glutamicum genome or can be
                                                                                                                                                                                                                                                                                                                                                         New isolated Corynebacterium glutamicum nucleic acid for production modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitami
Sequence
                                       used as markers for genetically engineered Corynebacterium or Brevibacterium. The HA proteins encoded by the (I) are used to maintain homeostasis in C. glutamicum or help the microorganism to adapt to
                                                                                                                                                                                                                                                                                                                Claim 20;
                                                                                                                                                                                                                                                                                                                                                or enzymes -
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DB; AAF71357.
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                            environmental conditions.
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99DE-1041378
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                             analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and procesus sequences from the Coryneform bacterium Corynebacterium glutamicum. These sequences from the Coryneform bacterium, or a gene derived from a mutant of coryneform bacterium, measuring expression amount and mutant of coryneform bacterium, measuring expression amount and gene derived
                                                                                             AAB93086 standard; Protein; 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression
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           Human protein sequence SEQ ID NO:11926
                                      26-JUN-2001 (first entry)
                                                                   AAB93086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                                                                                                                                         Sequence
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Tateishi N,
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DB; AAH65760.
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2000JP-0159162.
2000JP-0280988.
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Senoh A, Ikeda
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da M,
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Ozaki A;
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11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-off primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end
                                                                                                                                                                                          the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 represent human amino acid sequences; AAB92446 to AAH3633 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                          sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                             of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy.
   18
                                 4 PPPPLPPA 11
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pppplppa
                                                                  8
                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai T, Nishikawa T, Hayashi K, (
, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                586
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                   Conservative
                                                                                                                                                AA;
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                                                                   Mismatches
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(, Otsuki
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Title: US-09-485-529-103
Perfect score: 13
Sequence: 1 LNAPPPPLPPAPQ 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Query Match

61.5%; Score 8;

DB 2; Length 564;

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
									53.8			53.8			53.8	53.8
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	T14316	T31420	A36858	S24407	T18235	T19673	S50536	T30930	S19595	FOMVGM	QRHUP	T46412	I51691	T26998	D96711	T04832
•	rig-1 protein - mo	C-terminal domain-	G2R protein - vari	formin isoform IV	transcription acti	hypothetical prote	hypothetical prote	hypothetical prote	chloride channel p	gag-abl polyprotei	progesterone recep	ubiquitinprotein	dishevelled homolo	hypothetical prote	hypothetical prote	probable serine/th

## ALIGNMENTS

RESULT 2 T45866 T45866 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 C;Accession: T45866 R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mew submitted to the Protein Sequence Database, December 1999 A;Reference number: Z23007 A;Accession: T45866 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-564 <bar> A;Cross-references: EMBL:AL132978 A;Cross-references: EMBL:AL132978 A;Cross-references: EMBL:AL132978 A;Cross-references: EMBL:AL132978 A;Cross-references: EMBL:AL132978 A;Enerimental source: cultivar Columbia; BAC clone F3A4 C;Genetics: A;Map position: 3 A;Note: F3A4.210</bar>	Ouery Match  Best Local Similarity 100.0%; Pred. No. 1.5;  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps  Qy 2 NAPPPPLP 9                     Db 415 NAPPPPLP 422	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-443 <min> A;Cross-references: EMBL:U50197; PIDN:AAA91257.1; CESP:F25E2.4 A;Experimental source: strain Bristol N2 C;Genetics: A;Gene: CESP:F25E2.4 A;Gene: CESP:F25E2.4 A;Introns: 72/3; 110/3; 143/2; 171/3; 330/3; 385/3</min>	RESULT 1 T29820 hypothetical protein F25E2.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T29820 R;Minx, P.; Le, T. submitted to the EMBL Data Library, March 1996 A;Description: The sequence of C. elegans cosmid F25E2. A;Reference number: Z20691 A;Accession: T2920
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A;Molecule type: DNA
A;Residues: 1-1032 <STO>
A;Cross-references: GB:AE004446; GB:AE004091; NID:g9945886; PIDN:AAG03464.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
                                                                             Query Match
Best Local Similarity
Thehes 8; Conserv
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R;Stover, C:K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
""" B; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                            A; Gene: ppkA; PA0074
                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96636
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-907 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serine/threonine protein kinase PpkA PA0074 [imported] - Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005173; NID:g6751696; PIDN:AAF27679.1; GSPDB:GN00141
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       337
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  PPPPLPPA 344
                                                 PPPPLPPA 11
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                                                                                                     Conservative
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                                                                                                                            61.5%;
100.0%;
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0; Mismatches
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K.; Lim,
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
Atuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A.Authors: Hunter, J.C.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
glutaredoxin-like protein - Arabidopsis thaliana N;Alternate names: protein F14F18.100 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                  RESULT
T48552
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A; Map position: 1
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Best Local Similarity
"~+~hes 8; Conserv
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A;Experimental source: brain
C;Genetics:
A;Note: KIAA0595
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A;Molecule type: mRNA
A;Residues: 1-1520 <NAG>
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A;Title: Prediction of the coding sequences of unidentified human genes. IX. The comp A;Reference number: Z14086; MUID:98290545
A;Accession: T00273
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C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
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A; Accession: C96734
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Residues: 1-138 <STO>
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100.0%; F
tive 0;
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100.0%; Pred. No. 4.2;
Live 0; Mismatches
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Pred. No. 4.
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Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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51 N
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Khaykin, E.; Kim, Maiti, R.; Marzia

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Indels

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T48552

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submitted to the Protein Sec
A; Reference number: Z24490
A; Resession: T48552
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-145 <BEV>
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #t.
C;Accession: I51382
R;Jasoni, C.L.; Walker, M.B.; Morris, M.D.; Reh, T.A.
Development 120, 769-783, 1994
A;Title: A chicken achaete-scute homolog (CASH-1) is A;Reference number: I51382; MUID:95324365
A;Accession: I51882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL163812
A;Experimental source: cultivar Columbia; BAC clone F14F18
C;Genetics:
                                                                                                                                                                            R;Graves, T.; Sutterer, C.; Hawkins, M.; Wilson, R. submitted to the EMBL Data Library, January 1998 A;Description: The sequence of C. elegans cosmid C34B2. A;Reference number: Z21241 A;Accession: T32889
                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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  A; Map position:
A; Introns: 35/3
                                       A; Gene:
                                                                            A;Cross-references: EMBL:AF043693; PIDN:AAB97541.1; GSPDB:GN00019; CESP:C34B2.9
A;Experimental source: strain Bristol N2; clone C34B2
                                                                                                                    A; Molecule type: DNA
A; Residues: 1-238 <GRA>
                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                          hypothetical protein C34B2.9 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U01339; NID:g401726; PIDN:AAC59658.1; PID:g401727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-219 <JAS>
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A; Note: F14F18.100
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                                                                                                                                                                                                                                                                                Accession: T32889
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                                       CESP:C34B2.9
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10n: 1
35/3; 91/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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  200/2
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100.0%; Pred. No.
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6.3;
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Query Match

53.8%;

Score

7;

DB 2;

Length 238;

A;Status: preliminary; translated from GB/EMBL/DDBJ

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A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456
A;Clderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.;
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in Reference number: I38534; MUID:95105731
A;Accession: I38554
A;Accession: I38554
                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431 R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamu Blochem. Blophys. Res. Commun. 204, 468-474, 1994 A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection. A;Reference number: JC2340; MUID:95071350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species A;Reference number: I38707; MUID:95127560
A;Accession: I38707
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17312
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T17312
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A;Experimental source: adult testis; clone DKFZp434H018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-253 <OTT>
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A; Accession: T17312
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                                                                                                                                                                                                                                                                                                                    R; Schatzlein, C.E
                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g136990
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A; Residues: 1-281 <MIT>
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tive 0; Mismatches
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; Pred. No.
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                                                                                                                    Falk, B.; Schooley, K.A.;
                                                                   human T lymphocytes.
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R;Sulston, J.
submitted to the EMBL Data Library, June 1994
A;Reference number: Z19007
A;Accession: T18689
A;Accession: T18689
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A; Molecule type: DNA
A; Residues: 1-285 <WIL>
A; Cross-references: EMBL: Z34533; PIDN: CAA84294.1; GSPDB: GN00021; CESP: B0285.2
                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-289 < SCH>
A;Cross-references: EMBL:AL442043; GSPDB:GN00116; NCSP:B11E6.30
A;Experimental source: BAC clone B11E6; strain OR74A
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Best Local Similarity
Thehes 7; Conservi
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Best Local Similarity
"atches 7; Conservations
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C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted
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A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
                                                                                                                                                                                                                                                                                               C;Species: Neurospora crassa
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change
                                                                                                                                                                                                                A; Reference number: 226053
A; Accession: T52354
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A; Introns: 65/2; 131/2;
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                                                                                                                                                                                                                                                                R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
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                                                                                                                                                                                                                                                                                                                                 hypothetical protein Bl1E6.30 [imported] - Neurospora crassa
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                               Genetics:
                                                                                                                                                                                                                                                                               Accession: T52354
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               Query Match
Best Local
   Matches
                                                                                position:
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Local Similarity nes 7; Conserv
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                                                                                NCSP:BllE6.30 psition: 6
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               53.8%;
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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A;Introns: 17/2; 50/3; 333/2
A;Note: EG:34F3.10
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A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17685
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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METONI G., Reymond A., Alcalay M., Borsani G., Tanigami A.,
Meroni G., Reymond A., Alcalay M., Borsani G., Tanigami A.,
Tonlorenzi R., Lo Nigro C., Messali S., Zollo M., Ledbetter D.H.,
Brent R., Ballabio A., Carrozzo R.;
Brent R., Ballabio A., Carrozzo R.;
Brent R., Ballabio A., Carrozzo R.;
Rox, a novel bHLMZip protein expressed in quiescent cells that
heterodimerizes with Max, binds a non-canonical E box and acts as a
transcriptional repressor.";
EMBO J. 16:2892-2906(1997).
-I- FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES
-I- FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
CONFLICT
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DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNT_MOUSE STANDARD; PRT; 508789; P97349; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence up 15-DEC-1998 (Rel. 37, Last annotation MAX BINDING PROTEIN MNT (ROX PROTEIN) MNT OR ROX.
                                                                                 This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Multigene family.
                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           Hurlin P.J., Queva C., Elsenman R.N.; "Mnt, a novel Max-interacting protein is coeproliferating cells and mediates repression Genes Dev. 11:44-58(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00338; BRLZ;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97152466; PubMed-9000049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00036; BZIP_BASIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                         TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE 5'-CACGTG-3' AND, WITH HIGHER AFFINITY, TO 5'-CACGCG-3'.

SUBJUNT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX.

SUBCELLULAR LOCATION: NUCLEAR.

SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ņ
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U77356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR01217; PRICHEXTENSN PD004952; Hamlp_like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123
186
210
236
161
282
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llarity 100.0%;
Conservative
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194
230
250
163
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DNA-binding; Activator; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 0.0
0; Mismatches
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POLY-PRO.
BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEUCINE-ZIPPER
LLA -> RHE (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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                                                                      as
                                      http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTAGONIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROBABLE).
REF. 3).
                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 282;
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RESULT 3
GAG_MLVAB
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Best Local S
Matches 8
      InterPro; IPR000840; Gag_MA.
InterPro; IPR002079; Gag_P12.
InterPro; IPR003036; Gag_P30.
Pfam; PF01140; gag_MA; 1.
Pfam; PF01141; gag_P12; 1.
Pfam; PF02093; Gag_P30; 1.
                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  GAG_MLVAB
P03333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                      This SWISS-PROT entry is copyright. It is produced through a copyrend the swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GAG POLYPROTEIN CONTAINS: CORE PROTEIN P15;
                                                                                                                                                                                                                                                                                                                              Abelson murine leukemia virus.
Viruses; Retroid viruses; Retr
                                                                                                                                                                                                                                                                                                                                                              CORE SHELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1
                                                                          PIR; A03931;
                                                                                   EMBL; V01541; CAA24781.1; -.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
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InterPro; IPR001092; HLH_dim.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=11788;
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J0036; HELIA_
20n regulation; Re
224 235
226 272
236 272
273 301
273 379 379
273 392 392
27CT 402 403
LICT 402 403
LICT 414 41
NELICT 455
NELICT 525
S58
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                                                                                                                                                                                              POLYPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00038; HELIX_LOOP_HELIX; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                              PROTEIN P30].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                          FOMVGM.
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  401,
                                                                                                                                                                                                                                                                                   PubMed=6304726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; 500
100.0%; Pred. No.
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repressor; Nuclear protein; DNA-binding.
BASIC MOTIF (POTENTIAL).
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                              Retroviridae; Mammalian type C retroviruses
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G -> A (IN REF. 2).

V -> A (IN REF. 2).

A -> P (IN REF. 2).

T -> A (IN REF. 2).

G -> A (IN REF. 2).

G -> A (IN REF. 2).
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T -> P (IN REF. 2).
V -> A (IN REF. 2).
EE -> QQ (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                        INNER COAT PROTEIN P12;
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                                                                                                                                                    no restrictions
                                                                                                                                                               a collaboration - MBL outstation
                                                                                                                               for
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protein;

Polyprotein; Myristate

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Best Local S
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                                Matsumura M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE TOLELS, OR BOTH.
                                                                                                                                                                                                                                              "Role of Fas
infection.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FASL_HUMAN P48023;
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CHAIN
CHAIN
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Schaetzlein C.E., Poehlmann
Submitted (JUN-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95127560; PubMed-7826947;
Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
"Human Pas ligand: gene structure, chromosomal location and species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFSF6 OR APTILG1 OR FASL.
                                                                                                                                      TISSUE=Blood;
                                                                                                                                                   SEQUENCE OF 1-10 FROM N.A.
                                                                                                                                                                               Submitted
                                                                                                                                                                                        Wilkinson
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 204:468-474(1994)
                                                                                                                                                                                                                                                                                            MEDLINE=95071350;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alderson M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                           infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphocytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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           T CELLS, OR BOTH.
SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II MEMBRANE
                                                                                                                                                                                                                                                                             E., Hayashi N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPPLPP 10
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Similarity 100.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Med. 181:71-77(1995).
                                                                                                                                                                            (MAY-1997) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mediates activation-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
216
216
EXTRACELLULAR FLUID, PROBABLY
                                                                                                                                                                                                                                                    ligand in apoptosis induced by hepatitis C virus
                                                                                                                                                                                                                                                                   Kamada
                                                                                                                                                                                                                                                                                                                                                                               6:1567-1574(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                          PubMed=7980502;
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215
235
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                                                                                                                                                                                                                                                                                                                               R., Philippsen P., Eibel H. EMBL/GenBank/DDBJ databases
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                                                                                                                                                                            EMBL/GenBank/DDBJ databases
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Pred, No. 3.9
0; Mismatches
                                                                                                                                                                                                                                                                            Takehara T., Hijioka T., Kasahara A.,
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INNER COAT PROTEIN
CORE SHELL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4D83F71D7E056C7D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell death in human
             PROTEIN. MAY BE RELEASED
BY CLEAVAGE FORM THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (APTL).
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; Homo.
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Best Local (
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01-NOV-1995 (Rel. 32, Cr.
01-NOV-1995 (Rel. 32, La
01-NOV-1995 (Rel. 32, La
01-NOV-1995 (Rel. 32, La
пуротнетисац 31.4 кра р
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine; Transmembrane; G
DOMAIN 1 102
DOMAIN 81 102
DOMAIN 103 281
DOMAIN 4 70
DOMAIN 45 65
DISULTED 202 233
CARBOHYD 184 184
CARBOHYD 250 250
CARBOHYD 260 260
                                                                                                                                                                                                                                                                                                  CAEEL
            the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
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EMBL; U08137; AAC50071.1; --
EMBL; U1821; AAC50124.1; --
EMBL; D38122; BAA07320.1; --
EMBL; D36050; CAB09424.1; --
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 entities
                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                   Eukaryota; Metazoa;
Rhabditidae; Pelode:
                                                                                                                                                                                          Caenorhabditis elegans.
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                                                                                       Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                       Sulston
                                                                                                                                                      NCBI_TaxID=6239;
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InterPro; IPR000478; TNF_family.
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SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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requires a license agreement (See http://www.isb-sib.ch/announce/
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100.0%; Pr
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PROTEIN B0285.2 IN CH
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
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D (GLCNAC. ..)
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IN CHROMOSOME III
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Matches 7
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                                                                                                                                    Proc.
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MEDLINE-97264340; PubMed-9110173;
Didonato C.J., Chen X.N., Noya D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P97801: 009092;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SURVIVAL MOTOR NEURON PROTEIN.
                                                                                                                                                   mouse
                                                                                                                                                                        Schrank B., Goetz R., Gunnersen J.M. Smith A.G., Sendtner M.; "Inactivation of the survival motor
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Brain;
                                                                                                                                                                                                                                                                                      gene.";
                                                                                                                                                                                                                                                                                                 motor neuron gene: homolog
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                                                                                                                                                                                                                                                                          Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                     Viollet L., Bertrandy S., Brunialti A.L.B., Lefebvre S., Burlet P., Clermont O., Cruaud C., Guenet J.-L., Munnich A., Melki J.; "CLNA isolation, expression, and chromosomal localization of the mouse survival motor neuron gene (Smn).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97224505; PubMed=9070939;
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DOMAIN
                                                                                                                                                                                                                                                                                                                *Cloning, characterization,
                                                                                                                                                                                                                                                                                                                              Simard L.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10090;
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                                    C. Natl. Acad. Sci. U.S.A. 94:9920-9925(1997).

FÜNCTION: THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPLICEOS SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNI SPLICING IN THE NUCLEUS (BY SIMILARITY).

SPLICING IN THE NUCLEUS (BY SIMILARITY).

SUBJUNIT: FORMS A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF NEURON PROTEIN A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF NEURON PROTEIN A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF NEURON PROTEIN A STABLE HETEROMERIN 1 (SIPI/GEMIN2), GEMIN3 AN GEMIN4. THIS COMPLEX IS THOUGHT TO PLAY AN ESSENTIAL ROLE IN BIGGENESIS OF THE SMALL NUCLEAR RIBONUCLEOPROTEIN PARTICLES
(SNRNPS). INTERACTS WITH FIBRILLARIN AND WITH SEVERAL SPLICEOSOMAL SNRNP CORE SM PROTEINS, INCLUDING B/B^\prime, SM D AND SM E PROTEINS (BY SIMILARITY).
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                                                                                                                                       embryos."
                                                                                                                                                             spinal muscular atrophy,
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                   spinal muscular atrophy-determining
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s to massive cell death in
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tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).

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MGD; MGI:109565; Wbp7 InterPro; IPR000637;

EMBL;

U92455; AAC53192.1; -.

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20-AUG-2001 (Rel.
20-AUG-2001 (Rel.
TRITHORAX HOMOLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            proline-rich ligands.";
EMBO J. 16:2376-2383(1997).
-!- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR
                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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EMBL; U77714, AAC53144.1; -.
EMBL; Y1885; CAA73356.1; -.
MGD; MGI:109257; Smm.
MGD; MGI:109257; Tmm.
Integracy IPR02999; Tudor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97315177; PubMed=9171351;
Bedford M.T., Chan D.C., Leder P.;
"FBP WW domains and the Abl SH3 domain bind
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Mammalia; Eutheria; Rodentia;
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Mus musculus (Mouse)
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2 (WW DOMAIN BINDING PROTEIN 7) (FRAGMENT).
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Pred. No.
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MEDLINE-96051387; PubMed=7584026;

Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,

Sato S., Nagase T., Seki N., Ishikawa K.-I., Tahata S.;

"Prediction of the coding sequences of unidentified human genes. I.

The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by

The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by

analysis of randomly sampled cDNA clones from human immature myeloid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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(Rel. 40, Last ann
PROTEIN KIAA0009.
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SEQUENCE
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autocrine growth and monocyte differentiation.", Cell 91:185-195(1997).
-i- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR.
AND DIFFERENTIATION IN THE EMBRYO.
                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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SIGNAL
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTS AS A VIRULENCE FACTOR ACTIBE IN PLANT
                                                                                    SEQUENCE FROM N.A.

MEDLINE=98004222; PubMed=9346236;

KOWenz-Leutz E., Herr P., Niss K., Leutz A.;

"The homeobox gene GBX2, a target of the myb
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042230;
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                                                                                                                                                                                                                                                                                                                                                                 and Brain-Specific Homeobox
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                            FACTOR.
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                            FOR
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                         CELL PLURIPOTENCY
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                                                                                           mediates
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TWENT TO COLOR OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
NDPP_MC
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDPP_MOUSE
Q03173;
Q1-OCT-1996
Q1-OCT-1996
Q1-OCT-1996
                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  Sazuka T., Tomooka Y., Kathju S., Ikawa Y., Noda M., Kumar S.;
"Identification of a developmentally regulated gene in the mouse
central nervous system which encodes a novel proline rich protein.",
Blochim. Blophys. Acta 113:2240-248(1992).
-I- FUNCTION: MAY PLAY AN IMPORTANT BIOLOGICAL ROLE IN THE
DEVELOPMENT AND DIFFERENTIATION OF THE CENTRAL NERVOUS SYSTEM.
-I- TISSUE SPECIFICITY: IN THE HEART AND TESTIS AND LESS SO IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D10727; BAA01570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93041923; PubMed=1420303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF022151; AAB82710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLPPAP 75
                           MGI:97291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLPPAP 12
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                                                                                                                                                                                                                                                                                                                                          SKELETAL MUSCLE, KIDNEY, PANCREAS AND BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation updat
PROLINE RICH PROTEIN 1 (NDPP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 5.5;
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B71423225904E741 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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GSPT_HEADLY
ID GSPT_HEAD
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AC 014556
DT 30-MAY
DT AMMORIA
RA GARCÍA
CC -!- SU
CC -!- 
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Best Local :
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carrano A.V.:
Submilted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + C
+ NAD(+) - 1,3-DIPHOSPHATEGLYCERATE + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PUTATIVE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-SPECIFIC
                                                       ACT_SITE
                                                                                                         BINDING
                                                                                                                                                         Pfam; PF00044; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                             EMBL; AJ005371; CAA06501.1; -. EMBL; AC002389; AAB64181.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McLaughlin E.A., Hall L.;
"Nucleotide sequence of human testis-specific glycerald phosphate dehydrogenase (GAPDH-2) cDNA.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             014556; 060823;
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                                                                                                                                                                                                                                                           InterPro; IPR000173; GAP_DH.
InterPro; IPR002965; P_rich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHMAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS. SUBUNIT: HOMOTETRAMER (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY). SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2.1.12) (GAPDH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEHYDROGENASE FAMILY.
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quan G., Montgomery M., Ow
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                                                                                                                                    Oxidoreductase; NAD
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163
273
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276
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Primates;
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100.0%;
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(GAPDH-2) cDNA.";
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(BY SIMILARITY).
S -> SVDA...
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                                                  GLYCERALDEHYDE 3-PHOSPHATE (BY SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ARG. EE36C1CBE8156033 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adamson A.W., Burkhart-So., Stilwagen S., Garnes J.
M., Ow D., Kobayashi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-PRO.
LEU/PRO-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burkhart-Schultz K.,
., Garnes J., Dangana
bayashi A., Olsen A.O
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В
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Matches 7; Conser
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ALF_PETHY
O22621;
30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I: Solanales Colemnia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest
tree hv non-profit institutions as long as its content
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MEDLINE=98167899; PubMed=9435293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petunia hybrida (Petunia).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Activator; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF030171; AAC49912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petunia inflorescence development."; Development 125:733-742(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koes R.;
"Genetic control of branching pattern and
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                          Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01698; FLO_LFY;
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002910; FLO_LFY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
35
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                                      4
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SIMILARITY: BELONGS TO THE FLO / LFY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: PROBABLE TRANSCRIPTION FACTOR RE SPECIFICATION OF FLORAL MERISTEM IDENTITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                      PPPPLPP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPPLPP 60
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                                                                                 Conservative
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39,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                               Score 7; DB 1; Pred. No. 6.5
                                                                                 0;
                                                                                                                                                                                                                                                        POLY-GLU.
                                                                                                                                                                                    POLY-GLY.
POLY-ALA.
; F1C02FE8EB95AB33 CRC64;
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Pred. No.
                                                                                                                                                                                                                                                                                               POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spelt C., Bliek M., Mol J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                   DB 1;
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80

Matches Query Match Best Local

Similarity 7; Conserv

Conservative

Score 7; Pred. No.

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. 8;

Length 431;

Mismatches

Indels

0;

Gaps

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CLUON S.V., Eighmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares S., Squares S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
L. Nature 393:537-544(1998)."
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PKNA_MYCTU
                                                                                      NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKNA_MYCTU P71585;
                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE SERINE/FHREONINE-PROTEIN KINASE PKNA
PKNA OR RV0015C OR MT0018 OR MTCY10H4.15C.
                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                   Complete proteome.
DOMAIN 13
                                                                                                                                                                               Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                               InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_kin_actsite.
                                                                                                                                                                                                                                                                                                   TubercuList; Rv0015c;
                                                                                                                                                                                                                                                                                                                                                EMBL; Z80233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CDC 1551 / Oshkosh;
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NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                     Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                TIGR; MT0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole genome comparison
                                                                                                                                                                                                                                                                                                                              Z80233; CAB02435.1; -. AE006916; AAK44240.1;
                                                                                                                                                                                                  '00069; pkinase; 1.

PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PS00108; PROTEIN_KINASE_ST; 1.

PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                     253
27
42
141
53.8%; 5c.
100.0%; Pr
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                                                                                    ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
; 582D183747F3C111 CRC64;
                                                                                                                                                    PROTEIN KINASE.
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Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris D.,
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RESULT 15
GAA6\_HUMAN

В

233 PPPPLPP 239

0

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Query Match
Best Local Similarity
                                                          TRANSMEM
CARBOHYD
CARBOHYD
CARBOHYD
DISULFID
SEQUENCE
                                                                                                                                                                                    TRANSMEM
TRANSMEM
                                                                                                                                                      TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                       Pfam; PF00065; neur_chan; 2.
PRINTS; PR00252; NRIONCHANNEL.
PRINTS; PR00253; GABAARECEPTR.
PRINTS; PR01079; GABAARALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Q16445;
Q1-445;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last seguence update)
Q1-AUG-2001 (Rel. 40, Last annotation update)
QAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A))
                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                    PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
POSTSYNAPTIC membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-I- SIMILARITY: BELLONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haddingham K.L., Garrett E.M., Wafford K.A., Bain C., Heavens R.P., Sirinathsinghji D.J., Whiting P.J.; "Cloning of cDNAs encoding the human gamma-aminobutyric acid type receptor alpha 6 subunit and characterization of the pharmacology
                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; S81944; AAB36480.1; MIM; 137143; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha 6-containing receptors.";
Mol. Pharmacol. 49:253-259(1996).
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                                                                                                                                                                                                                                                                            Transmembrane; Multigene
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N-LINKED (GLCNAC. . .) (POTENTIAL).

BY SIMILARITY.

780F85845BCB107F CRC64;
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DB 1;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
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MEDLINE-99347734; PubMed=10421366;

Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,

Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F.,

Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;

"'Green revolution' genes encode mutant gibberellin response
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GIBBERELLIN RESPONSE MODULATOR.
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Nature 400:256-261(1999).
EMBL; AJ242531; CAB51555.1;
SEQUENCE 623 AA; 65337 M
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Triticum aestivum (Wheat).
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
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RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Janiel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pan S., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
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Best Local S
Matches
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O1-MAY-2000 (TrEMBLrel. 13,

O1-MAY-2000 (TrEMBLrel. 13,

O1-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D. Celniker S.E., Holt R.A., Evans C.R., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2000) to the EMBL; AP002866; BAB17094.1; SEQUENCE 66 AA; 7427 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10731132;
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Last annotation update)
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Pred. N
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Q99MA0;
01-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 17, L
01-JUN-2001 (TrEMBLrel. 17, L
TRANSCRIPTION FACTOR MRG2.
                                                                                                                                                                                                                                                                                                 Q9LW68;
Q9LW68;
Q1-OCT-2000
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EMBL; AE003595; AAF51766.1; -. ElyBase; FBgn0037118; CG14571.
Sato S., N
Submitted
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                    GB|AAC63835
                                                                                                                                                                                                                                                       01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evolution.";
Submitted (MAR-2001)
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Zhuang D.Z., Chou Y.-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                             STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                   SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural and functional conservation of MRG family in
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8; Conserv
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                        Nakamura Y.,
d (JUN-1998) t
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK30622.1;
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                     , Kaneko T.,
to the EMBL,
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                        o T., Kato T., Asamizu E., Tabata
EMBL/GenBank/DDBJ databases.
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Pred. No.
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Sciurognathi; Muridae
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. 0.54;
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udicots; Rosidae;
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RA Adams M.D., Celniker S.E., Richards S. Asiburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S. Asiburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burls N., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Borkova D., Herman S.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menther B., McIntosh T.C., McLeod M.P., McPherson D.
RA Menther B., C., Siden-Klamos I., Sumpson M., Skupski M.P., Smith T.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-COLUMBIA;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Q19782;
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Q1-NOV-1996 (TrEMBLrel. 01, Cr.
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EMBL; AEO03528; AAR49521.1; -
PlyBase; FBgn0036583; CG13055.
SEQUENCE 309 AA; 33224 MW; 9DAEB67784852A93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;

Minx P., Le T.;

Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U50197; AAA91257.1; -.

InterPro; IPR001664; IF.

Pfam; PF00038; filament; 2.

SEQUENCE 443 AA; 51881 MW; 286A54DDCB17730B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
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                                                                                                                                                               415 NAPPPPLP 422
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INTERMEDIATE FILAMENT. NCBI GI: 1213546
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         Waterston R.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
EMBL; AC004912; AAD15418.1; ..
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003124; WH2.
InterPro; IPR003124; WH2.
                                                                                                                                                                                                                                                                                                                                                                             095763 PRELIMINARY; PRT; 453 AJ 095763; 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequen 01-JUN-2001 (TrEMBLrel. 17, Last annota WUGSC:H_DJ0871B15.2 PROTEIN (FRAGMENT).
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                                                                                                                                                                                                  Bourne S., Wollam C., "The sequence of Homo Submitted (JUN-1998) t
                                                                                                                                                                                                                                                            MEDLINE-9963792; PubMed-9847074;
MEDLINE-9963792; PubMed-9847074;
Sulston J.E., Waterston R.;
"Toward a complete human genome sequence.";
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003124; WH2. Pfam; PF02205; WH2; 1. SMART; SM00246; WH2; 1. SEQUENCE 451 AA; 45307
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
SH3 DOMAIN BINDING PROTEIN.
                                                                                                        Submitted
                                                                                                                   SEQUENCE FROM N.A. Waterston R.H.;
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                     , Fielder T.; o sapiens PAC clone DJ0871B15."; to the EMBL/GenBank/DDBJ databases
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                                                                                                        EMBL/GenBank/DDBJ
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Pred. No.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6E2B50D1876E9CEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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; Murinae; Rat
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed in CNS neurons.";
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U31168; AAC99859.1; -.
R EMBL; U31161; AAC99859.1; JOINED.
EMBL; U31162; AAC99859.1; JOINED.
R EMBL; U31163; AAC99859.1; JOINED.
R EMBL; U31164; AAC99859.1; JOINED.
R EMBL; U31165; AAC99859.1; JOINED.
R EMBL; U31165; AAC99859.1; JOINED.
R EMBL; U31166; AAC99859.1; JOINED.
R EMBL; U31167; AAC99859.1; JOINED.
R EMBL; U31169; AAC99859.1; JOINED.
R EMBL; U31169; AAC99859.1; JOINED.
R EMBL; U31169; AAC99859.1; JOINED.
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Q920G8;
Q920G8;
Q1-MAY-1999 (TrEMBLrel. 10, C
Q1-MAY-1999 (TrEMBLrel. 10, L
Q1-JUN-2001 (TrEMBLrel. 17, L
SH3 DOMAIN BINDING PROTEIN.
O9FU62;
Q9FU62;
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01-MAR-2001
P0013F10.12
P0013F10.12.
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PRINTS; PRO1218; PSTLEXTENSIN.
SMART; SM00246; WH2; 1.
NON_TER 1 1
SEQUENCE 453 AA; 46578 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-FISCHER 344; TISSUE-LIVER; Ashman W-H., Smith J.L., Cotman S.L., "Gene organization and differential spread of the state o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR16.
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PRINTS; PRO1218; PSTLEXTENSIN.
SMART; SM00246; WH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003124; WH2.
InterPro; IPR003182; Pistil_extensin.
Pfam; PF02205; WH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100 nes 8; Conservative
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PROTEIN.
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                                                                                                                                                                                            PRELIMINARY;
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Rodentia;
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Pred. No. 1.1
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Pred. No.
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o. 1.2;
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. 1.1;
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CR16, a
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; Murinae; Rat
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O9W1X3;
O1-MAY-2000 (TIEMBLIEL 1
O1-MAY-2000 (TIEMBLIEL 1
O1-JUN-2001 (TIEMBLIEL 1
CG9848 PROTEIN.
CG9848.
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STRAIN-CV. NIFPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chr
clone:P0013F10.";
submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL; AP002523; BAB17066.1; -
SEQUENCE 507 AA; 53021 MW; 1BE50AFB7416444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II. Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
Hypothetical protein.
SEQUENCE 564 AA; 66602 MW; AD657
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Submitted (DEC-1999) to the
EMBL; AL132978; CAB62121.1;
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Bargues M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.

Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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nes 8; Conserv
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ilarity 100.0%;
Conservative
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Query Match
Best Local Similarity
"hehes 8; Conserv:
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Hank M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Butler H., Cadieu E., Colenter A., Chadra B.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
RA Berson K.Y., Benos P. Debrah R.D., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Colenter A., Chadra E.,
RA Gherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Colenter A., Chadra I.,
RA Gherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA Burtis K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dyan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Bessen C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegyam C.J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegyam C.J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegyam C.J., Ketchum K.A.,
RA Harris N., Moltra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N., Moltra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Maryen M., Nelson M., Strong R., Welson D.L.,
RA Harris N.L., Mang A., N., Nobarris J., Noshrefi A.,
RA Harris N.H., Weinson K.A., Navon K., Nusskard D.R., Pacleb J.M.,
Ra Harris N.H., Weins
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Search completed: January 22, 2002, 16:36:45
Job time: 345 sec
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No.
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Result
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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Compugen Ltd
                                                     Sequence 31, Appl
Sequence 356, App
Sequence 320, App
Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 2, Appli
Sequence 18, Appli
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US-08-769-745-31
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US-08-602-999A-356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 356, Application US/08602999A
; Patent No. 6184205
                                                                                                                 APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.

APPLICANT: QUILLIAM, Lawrence A.

APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.

APPLICANT: RIDER, James E.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METITLE OF INVENTION: ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity

Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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ADDRESSEE: Penn
STREET: 1155 Av
CITY: New York
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                               E: Pennie & Edmonds
1155 Avenue of the Americas
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US-08-652-877-22	US-08-336-343A-25	PCT-US95-03610-8	US-09-001-984C-34	US-08-899-595-8	US-08-900-321-8	US-08-212-190A-8	US-08-230-047-12	US-08-612-857-8	PCT-US94-01840-11	US-08-769-745-26	US-08-230-047-40	US-08-093-453B-2	US-07-945-283-2	US-09-170-996-28	US-09-170-996-12	US-08-609-049A-28	US-08-609-049A-12
Sequence 22, Appl	Sequence 25, Appl	Sequence 8, Appli	Sequence 34, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 12, Appl	Sequence 8, Appli	Sequence 11, Appl	Sequence 26, Appl	Sequence 40, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 28, Appl	Sequence 12, Appl	Sequence 28, Appl	Sequence 12, Appl

ALIGNMENTS

## Sequence 31, Application US/08769745 Patent No. 5955259 GENERAL INFORMATION: APPLICANT: Holmes, Todd C. APPLICANT: Levitan, Irwin B. APPLICANT: Brandeis University TITLE OF INVENTION: Mechanism for the Regulation of TITLE OF INVENTION: Channel Activity ; SOFTWARE: FastSEQ for Windows Version ; SEQ ID NO 31 ; LENGTH: 15 ; TYPE: PRT ; ORGANISM: Homo sapien US-08-769-745-31 FILE REFERENCE: BRU96-02 CURRENT APPLICATION NUMBER: US/08/769,745 CURRENT FILING DATE: 1996-12-19 NUMBER OF SEQ ID NOS: 41 Conservative 100.0%; 53.8%; %; Score 7; DB 2 %; Pred. No. 0.2 0; Mismatches DB 2; o. 0.28; Length 15; 0; Indels 0,

Gaps

0

METHODS

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; MOLECULE TYPE: peptide US-08-602-999A-356
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 16-FEB-19
                               ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                     CITY: New York STATE: New Yor
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
REFERENCE/DOCKET NUMBER: 1101-202
                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 PPPPLPP 12
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10036-2711
                                                                                                                                                                                                                                                 New York
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
GY: unknown
                                                                                                                                                                                                                                                                                                    E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                              RIDER, James E.
VENTION: SH3 BINDING PEPTIDES AND METHODS OF VENTION: ISOLATING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                             DER, Channing J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUILLIAM, Lawrence A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THORN, Judith M.
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                                                                                                                                                                                                                                                                                                                                                                                                                           FOWLKES, Dana M.
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100.0%; Pr
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Pred. No.
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0.28;
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Query Match
Best Local Similarity
7; Conserve
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US-08-602-999A-320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 320, Application US/08602999A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS
TITLE OF INVENTION: ISOLATING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                    TELEFAX: (214, merex: 66141 PENNIE
                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/602,999A FILING DATE: 16-FEB-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                amino acid
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1155 Avenue of the Americas
                                                                                                                                                                                                                                   (212) 790-9090
(212) 869-9741/8864
               53.8%; Score 7; DB 4; ilarity 100.0%; Pred. No. 0.33; Conservative 0; Mismatches
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212) 869-9741/8864
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                                                Length 18;
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                                                                                          Sequence 58, Application US/08399411
Patent No. 5831008
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Zinc Finger Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 535-9001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                           CORRESPONDENCE ADDRESS:
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ZIP: 92122
                                                                                                                                                                                                                                                                                             15 PPPPLPP 21
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
CONTREE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4370 La Jo
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100 nes 7; Conservative
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4370 La Jolla Village Drive, Suite 700
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; Pred. No.
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NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 28
TYPE: PRT
ORGANISM: Rat
US-08-769-745-39
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                                                                  ; Sequence 58, Application US/08516859A
; Patent No. 6069231
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Matches
                                                                                                                                                                                                                                         Best Local Similarity 100 Matches 7; Conservative
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Holmes, Todd C.
APPLICANT: Levitan, Irwin B.
APPLICANT: Levitan, Irwin B.
APPLICANT: Brandels University
TITLE OF INVENTION: Mechanism for the Regulation of Ion
TITLE OF INVENTION: Channel Activity
FILE REFERENCE: BRU96-02
CURRENT APPLICATION NUMBER: US/08/769,745
CURRENT FILING DATE: 1996-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                 GENERAL INFORMATION: APPLICANT: Huang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
APPLICANT: Huang, Shi
TITLE OF INVENTION: R
TITLE OF INVENTION: Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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Local Similarity 100.0%; Pred. No. 0.
nes 7; Conservative 0; Mismatches
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amino acid
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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N: 530
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                                                                                                                                                                                                                                    53.8%; 5c.
100.0%; Pr/
0;
Zinc Finger Proteins
                Retinoblastoma Protein - Interacting
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NUMBER OF SEQUENCES:

106

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US-08-818-112-78
COUNTRY: U.S.,
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
"""FIM PC compatible
"""FEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 78, Application US/08818112 Patent No. 6290969
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APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/ACENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 7-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                  APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 PPPPLPP 21
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                                                                                                                                                                              STREET:
                                                                                                                                                                                                 ADDRESSEE:
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3Y: linear
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                                                                                                                                                                              6300 Columbia Center, 701 Fifth Avenue
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                   Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campbell & Flores LLP
                                                                                                                                                                                               SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                       Steven G.
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100.0%;
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; MOLECULE TYPE: US-08-850-961-12
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Best Local :
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                                                                                            TELEFAX: (510) 655-3542 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 6013517man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 93004:
                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/850,961
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 PPLPPAP 29
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STRANDEDNESS: sir
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                                TOPOLOGY:
                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2, Application US/08850961
6013517
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7; Conservative
                                              : 140 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Driver, David A.
VENTION: CROSSLESS RETROVIRAL VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Polo, Nicholas J.
Chada, Sunil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bodner, Mordechai
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                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                           (510) 601-3520
              protein
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US-08-850-961-10
                                                                                                                   RESULT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,961
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 6013517man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 930049.424C4 / 1147.005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                Sequence 2, Application US/08810453
Patent No. 5858990
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
APPLICANT: Walsh, Kenneth
TITLE OF INVENTION: FAS LIGAND COMPOSITIONS FOR TREATMENT OF
TITLE OF INVENTION: PROLIFERATIVE DISORDERS
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                               105 PPPPLPP 111
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CITY: Emeryville
STATE: California
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                               4 PPPPLPP 10
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P.O. Box 8097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Driver, David A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (510)
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                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                             Length 141;
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US-08-815-190A-2
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                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Oueen, Cary L.

APPLICANT: Schneider, William P

APPLICANT: Vasquez, Maximiliano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Fas Ligand Fusion Proteins of TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
          CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/614,584
                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                           APPLICATION NUMBER: US/OFILING DATE: 11-MAR-1997
                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 PPPPLPP 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                     CITY:
                                                                                                                                                                                                                                                                   STREET:
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San Francisco
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E: Wolf, Greenfield & Sacks, P.C.
Federal Reserve Plaza, 600 Atlantic Avenue
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Schneider, William P.
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13-MAR-1996
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APPLICANT: Dean, Nicholas M.

APPLICANT: Marcusson, Eric G.

TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-09-290-640-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-290-640-25
; Sequence 25, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                   US-09-479-524-3
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Best Local Similarity luv.
Thes 7; Conservative
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                     Sequence 3, Application US/09479524
Patent No. 6288350
GENERAL INFORMATION:
APPLICANT: Barbera-Guillem, Emilio
TITLE OF INVENTION: Polynucleotides For Inhibiting Metastasis And Tumor Cell Growth
FILE REFERENCE: B-37
             EARLIER FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: WordPerfect
SEQ ID NO 3
LENGTH: 281
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Best Local Similarity
Matches 7; Conserv
                                                                                                        CURRENT APPLICATION NUMBER: US/09/479,524
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: US 09/170,948
EARLIER FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: US 60/062,733
LENGTH: 28
TYPE: PRT
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REFERENCE/DOCKET NUMBER: 011823-006710US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)_576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                           50 PPPPLPP 56
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Search completed: January 22, 2002, 16:30:54 Job time: 274 sec

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